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OM protein - protein search, using sw model

Run on: June 27, 2006, 01:48:32 ; Search time 178 Seconds  
(without alignments)  
1446.896 Million cell updates/sec

Title: US-10-689-576-1  
Perfect score: 2941  
Sequence: 1 MARTTSQLYDAVPIQSSVVL.....RKIQSVWRQYQSHPDAAVQ 556

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2941	100.0	556	3 US-09-771-161A-245 Sequence 245, App
2	2941	100.0	556	4 US-10-190-012-1 Sequence 1, Appli
3	2941	100.0	556	4 US-10-376-554-6 Sequence 6, Appli
4	2941	100.0	556	4 US-10-704-921-14 Sequence 14, Appl
5	2941	100.0	556	5 US-10-473-127-1372 Sequence 1372, Ap
6	2941	100.0	556	5 US-10-473-127-1373 Sequence 1373, Ap
7	2941	100.0	556	5 US-10-473-127-1374 Sequence 1374, Ap
8	2941	100.0	556	5 US-10-473-127-1377 Sequence 1377, Ap
9	2941	100.0	556	5 US-10-473-127-1378 Sequence 1378, Ap
10	2941	100.0	556	5 US-10-473-127-1380 Sequence 1380, Ap
11	2941	100.0	556	5 US-10-473-127-1382 Sequence 1382, Ap

SEQ ID NO 245  
LENGTH: 556  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-245

Query Match 100.0%; Score 2941; DB 3; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTSSSTPPGIPGGSRQGPAMDGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTSSSTPPGIPGGSRQGPAMDGTAAEPRP 60  
Oy 61 GAGSLQHAQPPPOPRKGRPEDFKFGKILGSGSPSTVVLARELATSREYAIKILEKRIIHK 120  
Db 61 GAGSLQHAQPPPOPRKGRPEDFKFGKILGSGSPSTVVLARELATSREYAIKILEKRIIHK 120  
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDEKLYFGLSYAQGLKLYIRKIGSPDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDEKLYFGLSYAQGLKLYIRKIGSPDET 180  
Oy 181 CTRPYTASIVSALSYLHGKGIIRDLKPENILNEDMHIIQIDPOTAKVLSPEKQARAN 240  
Db 181 CTRPYTASIVSALSYLHGKGIIRDLKPENILNEDMHIIQIDPOTAKVLSPEKQARAN 240  
Oy 241 SFVGTAGYVSPPELLTEKSACKSSDLMALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Db 241 SFVGTAGYVSPPELLTEKSACKSSDLMALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLHPPFESVTWENLHQOTPPKLT 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGPKLHPPFESVTWENLHQOTPPKLT 360  
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSNIGYIHDLD 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSHSLSASDTGLPQRSNIGYIHDLD 420  
Oy 421 SNSFELDLOFSEDSKRLLEKQAQGNPNHQPVENNLILOQGVDPKRLGKLPARRQLLTT 480  
Db 421 SNSFELDLOFSEDSKRLLEKQAQGNPNHQPVENNLILOQGVDPKRLGKLPARRQLLTT 480  
Oy 481 GPHLYYDVPNVKVLKGBIPMSQSLRPAQJFKTFVHTPNRTTYLADPSGNAHKCRKIQ 540  
Db 481 GPHLYYDVPNVKVLKGBIPMSQSLRPAQJFKTFVHTPNRTTYLADPSGNAHKCRKIQ 540  
Oy 541 BVMRQRQYQSHPDAAVQ 556  
Db 541 BVMRQRQYQSHPDAAVQ 556

RESULT 2  
US-10-190-012-1  
Sequence 1, Application US/10190012  
Publication No. US20030108971A1  
GENERAL INFORMATION:  
APPLICANT: Alessi, Dario R

12	2941	100.0	556	5	US-10-473-127-1383	Sequence 1383, Ap
13	2941	100.0	556	5	US-10-473-127-1384	Sequence 1384, Ap
14	2941	100.0	556	5	US-10-723-860-2053	Sequence 2053, Ap
15	2941	100.0	556	5	US-10-689-576-1	Sequence 1, Appli
16	2941	100.0	556	5	US-10-509-599-28	Sequence 28, Appl
17	2838	96.5	535	5	US-10-473-127-1379	Sequence 1379, Ap
18	2682	91.2	506	5	US-10-473-127-1381	Sequence 1381, Ap
19	2202.5	74.9	468	5	US-10-473-127-1371	Sequence 1371, Ap
20	2202.5	74.9	468	5	US-10-473-127-1385	Sequence 1385, Ap
21	1900	64.6	361	4	US-10-664-421-106	Sequence 106, App
22	1900	64.6	361	5	US-10-941-635-107	Sequence 107, App
23	1710	58.1	319	5	US-10-473-127-1375	Sequence 1375, Ap
24	1710	58.1	319	5	US-10-473-127-1386	Sequence 1386, Ap
25	1486	50.5	285	4	US-10-217-574-13	Sequence 13, Appl
26	1486	50.5	285	4	US-10-217-555-13	Sequence 13, Appl
27	1227	41.7	238	3	US-09-771-161A-154	Sequence 154, App
28	1146.5	39.0	752	4	US-10-108-605-133	Sequence 133, App
29	1144.5	38.9	752	4	US-10-190-012-29	Sequence 29, Appl
30	1144.5	38.9	752	5	US-10-689-576-29	Sequence 29, Appl
31	1144.5	38.9	752	6	US-11-097-143-138	Sequence 138, App
32	1144.5	38.9	752	6	US-11-097-143-573	Sequence 573, App
33	1144.5	38.9	752	6	US-11-097-143-28173	Sequence 28173, A
34	1144.5	38.9	755	6	US-11-097-143-28170	Sequence 28170, A
35	973	33.1	539	6	US-11-097-143-28176	Sequence 28176, A
36	973	33.1	539	6	US-11-097-143-28179	Sequence 28179, A
37	940	32.0	636	3	US-09-205-658-160	Sequence 160, App
38	940	32.0	636	3	US-09-963-693-160	Sequence 160, App
39	935	31.8	632	3	US-09-205-658-159	Sequence 159, App
40	935	31.8	632	3	US-09-963-693-159	Sequence 159, App
41	917.5	31.2	473	4	US-10-369-493-13231	Sequence 13231, A
42	875.5	29.8	537	4	US-10-425-114-64801	Sequence 64801, A
43	872.5	29.7	537	4	US-10-425-114-67015	Sequence 67015, A
44	870.5	29.6	504	4	US-10-425-115-292727	Sequence 292727, A
45	846.5	28.8	628	4	US-10-369-493-22776	Sequence 22776, A

## ALIGNMENTS

RESULT 1  
US-09-771-161A-245  
Sequence 245, Application US/09771161A  
Patent No. US20020110811A1  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0

TITLE OF INVENTION: ENZYME  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Jaeckle Fleischmann & Muegel, LLP  
STREET: 39 State Street  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14614-1310  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/190,012  
FILING DATE: 05-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,667  
FILING DATE: 03-OCT-1997  
APPLICATION NUMBER: GB 9705462.1  
FILING DATE: 17-MAR-1997  
APPLICATION NUMBER: GB 9712826.8  
FILING DATE: 19-JUN-1997  
APPLICATION NUMBER: GB 9717253.0  
FILING DATE: 15-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Braman, Susan J  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 87792.97R421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-262-3640  
TELEFAX: 716-262-4133  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 556 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-190-012-1

Query Match 100.0%; Score 2941; DB 4; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTSSSTPPGIPGGSRQGPAMDGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVTRTSSSTPPGIPGGSRQGPAMDGTAAEPRP 60  
Oy 61 GAGSLQHAQPPPOPRKGRPEDFKFGKILGSGSPSTVVLARELATSREYAIKILEKRIIHK 120

Db 61 GAGSLQHAQPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRII 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Qy 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Qy 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Db 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Db 361 YLPAMSEDDSDCYGNYNLLSQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Qy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIJOMGPVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIJOMGPVDKRGKLFARRRQLLLTE 480
Qy 481 GPHLYYVDPVNKVLKGIIPWSQLRPAKJNFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPVNKVLKGIIPWSQLRPAKJNFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 3
US-10-376-554-6
Sequence 6, Application US/10376554
Publication No. US20030215849A1
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: PDPK1 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX03-017C
CURRENT APPLICATION NUMBER: US/10/376,554
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/361,196
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 556
TYPE: PRT
ORGANISM: Homo sapiens
US-10-376-554-6

Query Match 100.0%; Score 2941; DB 4; Length 556;

PRIOR APPLICATION NUMBER: 60/424777
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 556
TYPE: PRT
ORGANISM: Homo sapiens
US-10-704-921-14

Query Match 100.0%; Score 2941; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDGTAAERPR 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDGTAAERPR 60
Qy 61 GAGSLQHAQPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRII 120
Db 61 GAGSLQHAQPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRII 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Qy 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Qy 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Db 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Db 361 YLPAMSEDDSDCYGNYNLLSQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Qy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIJOMGPVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIJOMGPVDKRGKLFARRRQLLLTE 480
Qy 481 GPHLYYVDPVNKVLKGIIPWSQLRPAKJNFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPVNKVLKGIIPWSQLRPAKJNFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 5
US-10-473-127-1372

Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDGTAAERPR 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDGTAAERPR 60
Qy 61 GAGSLQHAQPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRII 120
Db 61 GAGSLQHAQPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRII 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Qy 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Qy 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Db 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Db 361 YLPAMSEDDSDCYGNYNLLSQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420
Qy 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIJOMGPVDKRGKLFARRRQLLLTE 480
Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPMHQPVENNLIJOMGPVDKRGKLFARRRQLLLTE 480
Qy 481 GPHLYYVDPVNKVLKGIIPWSQLRPAKJNFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Db 481 GPHLYYVDPVNKVLKGIIPWSQLRPAKJNFTFFVHTPNRTTYLMDPSGNAHWCKRIQ 540
Qy 541 EVWRQRYQSHPDAAVQ 556
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 4
US-10-704-921-14
Sequence 14, Application US/10704921
Publication No. US20040166099A1
GENERAL INFORMATION:
APPLICANT: Rao, Patricia
TITLE OF INVENTION: MOLECULES PREFERENTIALLY ASSOCIATED WITH EFFECTOR T CELLS
FILE REFERENCE: T1N-026CP
CURRENT APPLICATION NUMBER: US/10/704,921
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/467477
PRIOR FILING DATE: 2003-05-02

Sequence 1372, Application US/10473127
Publication No. US20040236091A1
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026M01
CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1372
LENGTH: 556
TYPE: PRT
ORGANISM: Homo sapiens
US-10-473-127-1372

Query Match 100.0%; Score 2941; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 9.2e-212;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDGTAAERPR 60
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGGSROGPAMDGTAAERPR 60
Qy 61 GAGSLQHAQPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRII 120
Db 61 GAGSLQHAQPPQPRKORPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRII 120
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180
Qy 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Db 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240
Qy 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Db 241 SFVOTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIIKLEYD 300
Qy 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Db 301 FPKFPPKARDLVEKLLVLDATKRLGCEMBOYGPLKAHPFESVTWENLHQOTPPKLT 360
Qy 361 YLPAMSEDDSDCYGNYNLLSQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420

Db 361 ||||| YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSLSASDTGLPQRSNSIEQYIHDL 420  
Qy 421 SNSELDLQFSEDEKRLLEKQAGGNPMHQPVENNLLQMGPDVKRKLFAARRQLLLE 480  
Db 421 SNSELDLQFSEDEKRLLEKQAGGNPMHQPVENNLLQMGPDVKRKLFAARRQLLLE 480  
Qy 481 GPHLYYDVPVNVKLGSI PWSQSLRPEAKNFKTFVHTPNRTYYLMDPSNAHWCKRIQ 540  
Db 481 GPHLYYDVPVNVKLGSI PWSQSLRPEAKNFKTFVHTPNRTYYLMDPSNAHWCKRIQ 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 6  
US-10-473-127-1373  
; Sequence 1373, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1373  
; LENGTH: 556  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1373

Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTSSSTPPGIPGGSRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTSSSTPPGIPGGSRQGPAMDGTAAAPRP 60  
Qy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKXHIK 120  
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKXHIK 120

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1374  
; LENGTH: 556  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1374  
Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTSSSTPPGIPGGSRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTSSSTPPGIPGGSRQGPAMDGTAAAPRP 60  
Qy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKXHIK 120  
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKXHIK 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSPDST 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSPDST 180  
Qy 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240  
Db 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240  
Qy 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIILEYD 300  
Db 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIILEYD 300  
Qy 301 PFEKFFPKARDLVEKLLVLDAATKRLGCEMGGYGPLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 PFEKFFPKARDLVEKLLVLDAATKRLGCEMGGYGPLKAHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSLSASDTGLPQRSNSIEQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSLSASDTGLPQRSNSIEQYIHDL 420  
Qy 421 SNSELDLQFSEDEKRLLEKQAGGNPMHQPVENNLLQMGPDVKRKLFAARRQLLLE 480  
Db 421 SNSELDLQFSEDEKRLLEKQAGGNPMHQPVENNLLQMGPDVKRKLFAARRQLLLE 480  
Qy 481 GPHLYYDVPVNVKLGSI PWSQSLRPEAKNFKTFVHTPNRTYYLMDPSNAHWCKRIQ 540  
Db 481 GPHLYYDVPVNVKLGSI PWSQSLRPEAKNFKTFVHTPNRTYYLMDPSNAHWCKRIQ 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 8  
US-10-473-127-1377  
; Sequence 1377, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:

Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSPDST 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSPDST 180  
Qy 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240  
Db 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240  
Qy 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIILEYD 300  
Db 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIILEYD 300  
Qy 301 PFEKFFPKARDLVEKLLVLDAATKRLGCEMGGYGPLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 PFEKFFPKARDLVEKLLVLDAATKRLGCEMGGYGPLKAHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSLSASDTGLPQRSNSIEQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSLSASDTGLPQRSNSIEQYIHDL 420  
Qy 421 SNSELDLQFSEDEKRLLEKQAGGNPMHQPVENNLLQMGPDVKRKLFAARRQLLLE 480  
Db 421 SNSELDLQFSEDEKRLLEKQAGGNPMHQPVENNLLQMGPDVKRKLFAARRQLLLE 480  
Qy 481 GPHLYYDVPVNVKLGSI PWSQSLRPEAKNFKTFVHTPNRTYYLMDPSNAHWCKRIQ 540  
Db 481 GPHLYYDVPVNVKLGSI PWSQSLRPEAKNFKTFVHTPNRTYYLMDPSNAHWCKRIQ 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 7  
US-10-473-127-1374  
; Sequence 1374, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041

; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1377  
; LENGTH: 556  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1377

Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTSSSTPPGIPGGSRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTSSSTPPGIPGGSRQGPAMDGTAAAPRP 60  
Qy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKXHIK 120  
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKXHIK 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSPDST 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSPDST 180  
Qy 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240  
Db 181 CTRPYTASIVSALEYLHGKGIHRDLKPENILLNEDMHIQITDPTAKVLSPEKQARAN 240  
Qy 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIILEYD 300  
Db 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFOKIILEYD 300  
Qy 301 PFEKFFPKARDLVEKLLVLDAATKRLGCEMGGYGPLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 PFEKFFPKARDLVEKLLVLDAATKRLGCEMGGYGPLKAHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSLSASDTGLPQRSNSIEQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSLSASDTGLPQRSNSIEQYIHDL 420

Db	121	SNKVPYVTRDERVMSRLDHPFPVKLYPTFDQDSKLVGLSTAQSGELLKYLKRGISPDST	180
Qy	181	CTRFYTAIVSALEYLHGKQIIIRHDLKPENILINEDGHQITQDPTAKVLSPESKQARAN	240
Db	181	CTRFYTAIVSALEYLHGKQIIIRHDLKPENILINEDGHQITQDPTAKVLSPESKQARAN	240
Qy	301	SPVGTAAQVSPPELLTEKSACKSSDIMALGCIIVQLVAGLPPFARGNYLIPKIIKLEYD	300
Db	301	SPVGTAAQVSPPELLTEKSACKSSDIMALGCIIVQLVAGLPPFARGNYLIPKIIKLEYD	300
Qy	361	FPBKFPFKARDVLKLLVLDATKRLGCSBMBGYGLKAPFPFESVTVNHLAQOTPKKLTA	360
Db	361	FPBKFPFKARDVLKLLVLDATKRLGCSBMBGYGLKAPFPFESVTVNHLAQOTPKKLTA	360
Qy	361	YLPAMSEDDQDCYGNYNLLSQPGCMQVSSSSSHSLASDUTGLPQSGSNIQYIHDL	420
Db	361	YLPAMSEDDQDCYGNYNLLSQPGCMQVSSSSSHSLASDUTGLPQSGSNIQYIHDL	420
Qy	421	SNSFELDLPSEDEKRLILLEKQAGGNPHQFVNNLILQMGVDIKRGLFARRQGLLTE	480
Db	421	SNSFELDLPSEDEKRLILLEKQAGGNPHQFVNNLILQMGVDIKRGLFARRQGLLTE	480
Qy	481	GPHLYYDVPNKVLKGIIPWSQSLRPEAQNFKTFFVHTPNRTYYLMDPSGNARWKCRKIQ	540
Db	481	GPHLYYDVPNKVLKGIIPWSQSLRPEAQNFKTFFVHTPNRTYYLMDPSGNARWKCRKIQ	540
Qy	541	SVWRQRYQSHPDAAVQ 556	
Db	541	SVWRQRYQSHPDAAVQ 556	

RESULT 10  
US-10-473-127-1380  
Sequence 1380, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycoo Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILI  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
CURRENT PRIORITY NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: PspSeq for Windows Version 4.0  
SEQ ID NO 1380  
LENGTH: 556

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:      LENGTH: 556

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:      LENGTH: 556

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1 CURRENT APPLICATION NUMBER: US/10/473,127
2
3 CURRENT FILING DATE: 2003-09-26
4
5 PRIOR APPLICATION NUMBER: 60/279,495
6
7 PRIOR FILING DATE: 2001-03-28
8
9 PRIOR APPLICATION NUMBER: 60/292,544
10
11 PRIOR FILING DATE: 2001-05-21
12
13 PRIOR APPLICATION NUMBER: 60/310,801
14
15 PRIOR FILING DATE: 2001-08-08
16
17 PRIOR APPLICATION NUMBER: 60/326,370
18
19 PRIOR FILING DATE: 2001-10-01
20
21 PRIOR APPLICATION NUMBER: 60/336,780
22
23 PRIOR FILING DATE: 2001-12-04
24
25 PRIOR APPLICATION NUMBER: 60/358,985
26
27 PRIOR FILING DATE: 2002-02-20
28
29 NUMBER OF SEQ ID NOS: 2041
30
31 SOFTWARE: GCG/SEQ for Windows Version 4.0
32
33 SEQ ID NO 1362
34
35 LENGTH: 556
36
37 TYPE: PRT
38
39 ORGANISM: Homo sapiens
40
41 US-10-473:127-1382

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Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MARTTSQLYDAVP	I	QSSVFLCS	CPSP	SMVTR	TQTS	SS	TPGI	PGGSRG	PAMD	TAA	PRP	60
Db	1	MARTTSQLYDAVP	I	QSSVFLCS	CPSP	SMVTR	TQTS	SS	TPGI	PGGSRG	PAMD	TAA	PRP	60
Qy	61	QAGSLQAHP	PPPO	PKR	KRP	DP	KFGK	IL	GGSG	FSTV	VLARE	LATS	RSRY	120
Db	61	QAGSLQAHP	PPPO	PKR	KRP	DP	KFGK	IL	GGSG	FSTV	VLARE	LATS	RSRY	120
Qy	121	ENKVPYV	TR	RDVMS	RLDHP	FF	VFKLY	TP	PDQDE	KLY	FG	LSY	AKNG	160
Db	121	ENKVPYV	TR	RDVMS	RLDHP	FF	VFKLY	TP	PDQDE	KLY	FG	LSY	AKNG	160
Qy	181	CRFPYTV	IAS	SLY	LAGKI	I	HRD	LKPEN	IL	LANE	DGH	IGI	TPD	240
Db	181	CRFPYTV	IAS	SLY	LAGKI	I	HRD	LKPEN	IL	LANE	DGH	IGI	TPD	240
Qy	241	SPVGTAG	YVS	PELL	TS	ES	ACKS	SD	ML	AG	LCI	I	YQ	300
Db	241	SPVGTAG	YVS	PELL	TS	ES	ACKS	SD	ML	AG	LCI	I	YQ	300

Db	241	5FVGTAQVVSPELLTEISACKSSDLMALOCIT1YGVAGLPFFPAGNSYLIPKIKLSTYD	300
Qy	301	FFKFFPKARDLVEKLLVLVDATKRLGCESEGYOPLKAPFFSYVWNLIAQOTPKKLTAT	360
Db	301	FFKFFPKARDLVEKLLVLVDATKRLGCESEGYOPLKAPFFSYVWNLIAQOTPKKLTAT	360
Qy	361	YLPAMSEDDDCVGYNNLLSQPGCMQVSSSSSSHLSAEDTGLPQSGNSIYIYHDL	420
Db	361	YLPAMSEDDDCVGYNNLLSQPGCMQVSSSSSSHLSAEDTGLPQSGNSIYIYHDL	420
Qy	421	SNISPELDQFSEDRKLLLETKAAGNPHWQVENVLLIHQGVYDVKRLPARRQLLTET	480
Db	421	SNISPELDQFSEDRKLLLETKAAGNPHWQVENVLLIHQGVYDVKRLPARRQLLTET	480

Qy 421 SNSFELOLOQFSEDEKRLLLSKAOGNPMHQFVENNLI LKMGFVDKRGKLPARRRQLLLTE 480  
Db 421 SNSFELOLOQFSEDEKRLLLSKAOGNPMHQFVENNLI LKMGFVDKRGKLPARRRQLLLTE 480

Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Db 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 12

US-10-473-127-1383  
; Sequence 1383, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1383  
; LENGTH: 556  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1383

Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVTRTQSSSTPPGIPGGSROGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVTRTQSSSTPPGIPGGSROGPAMDGTAAAPRP 60  
Qy 61 GAGSLQAQPPQPRKRPDPFKFKILGEGSFSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQAQPPQPRKRPDPFKFKILGEGSFSTVVLARELATSREYAIKILEKRII 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGELLYKIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGELLYKIRKIGSFDET 180  
Qy 181 CTRFYTAIVSALEYLHGKGI IHRDLKPENILLNEDMHQITDGTAKVLSPEKQARAN 240

Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVTRTQSSSTPPGIPGGSROGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVTRTQSSSTPPGIPGGSROGPAMDGTAAAPRP 60  
Qy 61 GAGSLQAQPPQPRKRPDPFKFKILGEGSFSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQAQPPQPRKRPDPFKFKILGEGSFSTVVLARELATSREYAIKILEKRII 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGELLYKIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGELLYKIRKIGSFDET 180  
Qy 181 CTRFYTAIVSALEYLHGKGI IHRDLKPENILLNEDMHQITDGTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGI IHRDLKPENILLNEDMHQITDGTAKVLSPEKQARAN 240  
Qy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI I KLEYD 300  
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI I KLEYD 300  
Qy 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBMBGYGLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBMBGYGLKAHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQRSNGNI EGYI HDLD 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQRSNGNI EGYI HDLD 420  
Qy 421 SNSFELDLPSEDSKRLLEKQAGGNPWHPVENNLI LKMGFVDRKGLFARRRQLLLTE 480  
Db 421 SNSFELDLPSEDSKRLLEKQAGGNPWHPVENNLI LKMGFVDRKGLFARRRQLLLTE 480  
Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Db 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 14

US-10-723-860-2053  
; Sequence 2053, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Azis, Nataasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

Db 181 CTRFYTAIVSALEYLHGKGI IHRDLKPENILLNEDMHQITDGTAKVLSPEKQARAN 240  
Qy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI I KLEYD 300  
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI I KLEYD 300  
Qy 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBMBGYGLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBMBGYGLKAHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQRSNGNI EGYI HDLD 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQRSNGNI EGYI HDLD 420  
Qy 421 SNSFELDLPSEDSKRLLEKQAGGNPWHPVENNLI LKMGFVDRKGLFARRRQLLLTE 480  
Db 421 SNSFELDLPSEDSKRLLEKQAGGNPWHPVENNLI LKMGFVDRKGLFARRRQLLLTE 480  
Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Db 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 13

US-10-473-127-1384  
; Sequence 1384, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1384  
; LENGTH: 556  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1384

; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2053  
; LENGTH: 556  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-723-860-2053

Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVTRTQSSSTPPGIPGGSROGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPSMVTRTQSSSTPPGIPGGSROGPAMDGTAAAPRP 60  
Qy 61 GAGSLQAQPPQPRKRPDPFKFKILGEGSFSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQAQPPQPRKRPDPFKFKILGEGSFSTVVLARELATSREYAIKILEKRII 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGELLYKIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGELLYKIRKIGSFDET 180  
Qy 181 CTRFYTAIVSALEYLHGKGI IHRDLKPENILLNEDMHQITDGTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGI IHRDLKPENILLNEDMHQITDGTAKVLSPEKQARAN 240  
Qy 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI I KLEYD 300  
Db 241 SPVGTAAQVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPPFRAGNEYLIFOKI I KLEYD 300  
Qy 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBMBGYGLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 PFEKFFPKARDLVEKLLVLDATKRLGCEBMBGYGLKAHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQRSNGNI EGYI HDLD 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQRSNGNI EGYI HDLD 420  
Qy 421 SNSFELDLPSEDSKRLLEKQAGGNPWHPVENNLI LKMGFVDRKGLFARRRQLLLTE 480  
Db 421 SNSFELDLPSEDSKRLLEKQAGGNPWHPVENNLI LKMGFVDRKGLFARRRQLLLTE 480  
Qy 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Db 481 GPHLYYDVPVNVKLGSI PWSQLRPEAKNPKTFVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 15  
US-10-689-576-1  
; Sequence 1, Application US/10689576  
; Publication No. US20050032185A1  
; GENERAL INFORMATION:  
; APPLICANT: Alessi, Dario R  
; TITLE OF INVENTION: ENZYME  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jaeckle Fleischmann & Muehl, LLP  
; STREET: 39 State Street  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14614-1310  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/689,576  
; FILING DATE: 20-Oct-2003  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,667  
; FILING DATE: 03-OCT-1997  
; APPLICATION NUMBER: GB 9705462.1  
; FILING DATE: 17-MAR-1997  
; APPLICATION NUMBER: GB 9712826.8  
; FILING DATE: 19-JUN-1997  
; APPLICATION NUMBER: GB 9717253.0  
; FILING DATE: 15-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brame, Susan J  
; REGISTRATION NUMBER: 34,103  
; REFERENCE/DOCKET NUMBER: 87792.97R421  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-262-3640  
; TELEFAX: 716-262-4133  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 556 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-689-576-1  
  
Query Match 100.0%; Score 2941; DB 5; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9.2e-212;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MARTTSOLYDAVPVIGSSVVLCSPPSPSWRTQTESSTPPGIPGSGRQGPAMQGTAAASPRP 60  
Db 1 MARTTSOLYDAVPVIGSSVVLCSPPSPSWRTQTESSTPPGIPGSGRQGPAMQGTAAASPRP 60  
Qy 61 GAGSLQHAQPPPPQPRKRPEDFKFGKILGEGSPSTVVLARELATSRFYIKILSKRHIIK 120  
Db 61 GAGSLQHAQPPPPQPRKRPEDFKFGKILGEGSPSTVVLARELATSRFYIKILSKRHIIK 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFOODEKLYPGLSYAKNGELLKYIRKIGSPDST 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFOODEKLYPGLSYAKNGELLKYIRKIGSPDST 180  
Qy 181 CTRPYTASIVSALEYLHGKDI IHRDLKPENILNEDKHIOITDPTAKVLSPEKQARAN 240  
Db 181 CTRPYTASIVSALEYLHGKDI IHRDLKPENILNEDKHIOITDPTAKVLSPEKQARAN 240  
Qy 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPFFRAGNSYLIFOKIIKLEYD 300  
Db 241 SFVGTAYVSPPELLTEKSACKSSDLWALGCI IYQLVAGLPFFRAGNSYLIFOKIIKLEYD 300  
Qy 301 FPKKFPKARDLVSKLLVLDATKRLGCESEMGYGLKQHPFFESVTWNLHQQTTPPKLTA 360  
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Qy 361 YLPAMSEDDDDCYGNVDNLLSQFGCMQVSSSSSSSLASDPTGLPQSGSNISQYIHDL 420  
Db 361 YLPAMSEDDDDCYGNVDNLLSQFGCMQVSSSSSSSLASDPTGLPQSGSNISQYIHDL 420  
Qy 421 SNSFELDLQFSEDEKRLLESKQAGNPWHQFVENNLI IJMGPVDKRKLFPARRQLLLTS 480  
Db 421 SNSFELDLQFSEDEKRLLESKQAGNPWHQFVENNLI IJMGPVDKRKLFPARRQLLLTS 480  
Qy 481 GPHLYYVDPVNKLKGEI PMSQSLRPAKNPKTFPVHTPNRTTYLMDPSGNAHWCRKIQ 540  
Db 481 GPHLYYVDPVNKLKGEI PMSQSLRPAKNPKTFPVHTPNRTTYLMDPSGNAHWCRKIQ 540  
Qy 541 EVWRORYQSHPDAAVQ 556  
Db 541 EVWRORYQSHPDAAVQ 556

Search completed: June 27, 2006, 01:51:45  
Job time : 180 secs

OM protein - protein search, using sw model

Run on: June 27, 2006, 01:36:37 ; Search time 51 Seconds  
(without alignments)  
954.255 Million cell updates/sec

Title: US-10-689-576-1  
Perfect score: 2941  
Sequence: 1 MARTTSQLYDAVPIGSSVVL.....RKIQEVQRQYQSHPDAAVQ 556

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87510628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2941	100.0	556 1 US-09-016-000-4	Sequence 4, Appli
2	2941	100.0	556 2 US-08-943-667-1	Sequence 1, Appli
3	2941	100.0	556 2 US-09-771-161A-245	Sequence 245, App
4	2937	99.9	556 2 US-09-156-793D-2	Sequence 2, Appli
5	1227	41.7	238 2 US-09-771-161A-154	Sequence 154, App
6	1144.5	38.9	752 2 US-08-943-667-29	Sequence 29, Appl
7	940	32.0	636 2 US-09-205-658-160	Sequence 160, App
8	935	31.8	632 2 US-09-205-658-159	Sequence 159, App
9	712	24.2	766 2 US-09-538-092-216	Sequence 216, App
10	655.5	22.3	901 2 US-09-248-796A-20495	Sequence 20495, A

CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,000  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0465 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 556 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: MOKLIDT01  
CLONE: 472480  
US-09-016-000-4

Query Match 100.0%; Score 2941; DB 1; Length 556;  
Best Local Similarity 100.0%; Pred. No. 1.4e+247;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIGSSVVLCSPPSMVKTOTSSSTPPGIPGGSQGPAMDOTAAEP RP 60  
Db 1 MARTTSQLYDAVPIGSSVVLCSPPSMVKTOTSSSTPPGIPGGSQGPAMDOTAAEP RP 60  
Qy 61 GAGSLQAQPPPPRIKGRPEDFKPKILGSGSPSTVVLARELATSREYA1KILSKKH1K 120  
Db 61 GAGSLQAQPPPPRIKGRPEDFKPKILGSGSPSTVVLARELATSREYA1KILSKKH1K 120  
Qy 121 ENKVPVVTRESDVMSRLDHPFFVKLYPTFQDEKLYPGLSYAJNGELLYKIRKIGSPDT 180  
Db 121 ENKVPVVTRESDVMSRLDHPFFVKLYPTFQDEKLYPGLSYAJNGELLYKIRKIGSPDT 180  
Qy 181 CTRPYTASIVSALEYLHGKQI1HRDLKPNILNEMDI1QITDPTAKVLSPSKQARAN 240  
Db 181 CTRPYTASIVSALEYLHGKQI1HRDLKPNILNEMDI1QITDPTAKVLSPSKQARAN 240  
Qy 241 SPVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPFRAGNEYLI1FKI1KLEYD 300

11 614 20.9 113 2 US-09-205-658-173 Sequence 173, App  
12 573 19.5 104 2 US-09-205-658-202 Sequence 202, App  
13 571.5 19.4 420 2 US-09-949-016-11701 Sequence 11701, A  
14 562 19.1 431 2 US-09-031-295-2 Sequence 2, Appli  
15 562 19.1 431 2 US-10-000-039-2 Sequence 2, Appli  
16 561 19.1 407 2 US-10-067-977-4 Sequence 4, Appli  
17 561 19.1 445 2 US-10-067-977-2 Sequence 2, Appli  
18 561 19.1 526 2 US-10-094-749-1861 Sequence 1861, Ap  
19 560.5 19.1 256 2 US-09-964-956-72 Sequence 72, Appl  
20 560.5 19.1 358 2 US-09-949-016-6582 Sequence 6582, Ap  
21 560.5 19.1 358 2 US-10-427-923-4 Sequence 4, Appli  
22 556 18.9 398 2 US-09-538-092-501 Sequence 501, App  
23 556 18.9 398 2 US-09-487-558B-404 Sequence 404, App  
24 555 18.9 430 1 US-08-712-709-9 Sequence 9, Appli  
25 555 18.9 430 2 US-09-111-444-9 Sequence 9, Appli  
26 555 18.9 430 2 US-09-541-228-9 Sequence 9, Appli  
27 554 18.8 380 2 US-09-487-558B-402 Sequence 402, App  
28 553 18.8 431 1 US-08-712-709-5 Sequence 5, Appli  
29 553 18.8 431 2 US-09-111-444-5 Sequence 5, Appli  
30 553 18.8 431 2 US-09-541-228-5 Sequence 5, Appli  
31 550.5 18.7 350 2 US-09-538-092-991 Sequence 991, App  
32 550.5 18.7 359 2 US-09-949-016-7862 Sequence 7862, Ap  
33 543 18.5 343 2 US-09-394-455-15 Sequence 15, Appl  
34 542 18.4 336 2 US-09-394-455-2 Sequence 2, Appli  
35 542 18.4 343 2 US-09-394-455-34 Sequence 34, Appl  
36 542 18.4 350 2 US-09-538-092-946 Sequence 946, App  
37 542 18.4 351 2 US-09-394-455-4 Sequence 4, Appli  
38 542 18.4 351 2 US-09-771-161A-194 Sequence 194, App  
39 540 18.4 343 2 US-09-394-455-38 Sequence 38, Appl  
40 540 18.4 595 2 US-09-417-197-69 Sequence 69, Appl  
41 539.5 18.3 541 2 US-09-205-658-154 Sequence 154, App  
42 538 18.3 350 2 US-09-457-040B-37 Sequence 37, Appl  
43 538 18.3 351 2 US-09-457-040B-6 Sequence 6, Appli  
44 537 18.3 260 1 US-07-857-224B-4 Sequence 4, Appli  
45 535.5 18.2 637 2 US-09-817-310-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-016-000-4  
; Sequence 4, Application US/09016000  
; Patent No. 5962232  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Bandman, Olga  
; APPLICANT: Akerblom, Ingrid E.  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive

Db 241 SPVGTAAQYVSPPELLTEKSACKSSDLWALGCI1YQLVAGLPFRAGNEYLI1FKI1KLEYD 300  
Qy 301 FPEKFFPKARDLVKLLVLQDATKRLGCSBHGYPGLKHPFFSVTWNH1HOOTPPK1TA 360  
Db 301 FPEKFFPKARDLVKLLVLQDATKRLGCSBHGYPGLKHPFFSVTWNH1HOOTPPK1TA 360  
Qy 361 YLPAMSEDDDCYGNVNLSPQGMQVSSSSSSSLASDVTGLPQRSN1E0Y1HDL0 420  
Db 361 YLPAMSEDDDCYGNVNLSPQGMQVSSSSSSSLASDVTGLPQRSN1E0Y1HDL0 420  
Qy 421 SNSFELDLQFSDEKRLLEKQAGGNPMHQPVENN1L1KMGPDVKRKLFPARRQLL1TE 480  
Db 421 SNSFELDLQFSDEKRLLEKQAGGNPMHQPVENN1L1KMGPDVKRKLFPARRQLL1TE 480  
Qy 481 GPHLYYVDVFNKVLKGSIPMSQSLRPEAKNFKTFVHTPNRTTYLADPSNAH1KWRK1Q 540  
Db 481 GPHLYYVDVFNKVLKGSIPMSQSLRPEAKNFKTFVHTPNRTTYLADPSNAH1KWRK1Q 540  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 2  
US-08-943-667-1  
; Sequence 1, Application US/08943667  
; Patent No. 6734001  
; GENERAL INFORMATION:  
; APPLICANT: Alessi, Dario R  
; TITLE OF INVENTION: ENZYMS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jaeschke Fleischmann & Muegel, LLP  
; STREET: 39 State Street  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14614-1310  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,667  
; FILING DATE: 03-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9705462.1  
; FILING DATE: 17-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9712826.8  
; FILING DATE: 19-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9717253.0  
; FILING DATE: 15-AUG-1997  
; ATTORNEY/AGENT INFORMATION:

NAME: Brennan, Susan J  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 87792,97R421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-262-3640  
TELEFAX: 716-262-4133  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 556 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEetical: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-943-667-1

Query Match 100.0%; Score 2941; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 1.4e-247;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTQTSSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTQTSSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Oy 61 GAGSLQHAQPPPPQPKRKPDPFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQHAQPPPPQPKRKPDPFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120  
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKGSELLKYIRKIGSPDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKGSELLKYIRKIGSPDET 180  
Oy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240  
Oy 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIKLEYD 300  
Db 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIKLEYD 300  
Oy 301 FPKFPPKARDLVEKLLVLADATKRLGCEMSEGYGLKAHPFFESVTWENLHQOTPPKLT 360  
Db 301 FPKFPPKARDLVEKLLVLADATKRLGCEMSEGYGLKAHPFFESVTWENLHQOTPPKLT 360  
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNIQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNIQYIHDL 420  
Oy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLPARRRQLL 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLPARRRQLL 480  
Oy 481 GPHLYYVDPVNKLKGSIPMSQSLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCCKIQ 540  
Db 481 GPHLYYVDPVNKLKGSIPMSQSLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCCKIQ 540

Db 301 FPKFPPKARDLVEKLLVLADATKRLGCEMSEGYGLKAHPFFESVTWENLHQOTPPKLT 360  
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNIQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNIQYIHDL 420  
Oy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLPARRRQLL 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLPARRRQLL 480  
Oy 481 GPHLYYVDPVNKLKGSIPMSQSLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCCKIQ 540  
Db 481 GPHLYYVDPVNKLKGSIPMSQSLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCCKIQ 540  
Oy 541 EVNRORYQSHPDAAVQ 556  
Db 541 EVNRORYQSHPDAAVQ 556

RESULT 4  
US-09-156-793D-2  
Sequence 2, Application US/09156793D  
Patent No. 6682920  
GENERAL INFORMATION:  
APPLICANT: Stephens, Len  
APPLICANT: Hawkins, Philip T.  
APPLICANT: Stokoe, David  
TITLE OF INVENTION: Compositions and Methods for Identifying PKB Kinase  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE: 1030-US  
CURRENT APPLICATION NUMBER: US/09/156,793D  
CURRENT FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/060,190  
PRIOR FILING DATE: 1997-09-26  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 2  
LENGTH: 556  
TYPE: PRT  
ORGANISM: PKB Kinase  
US-09-156-793D-2

Query Match 99.9%; Score 2937; DB 2; Length 556;  
Best Local Similarity 99.8%; Pred. No. 3.2e-247;  
Matches 555; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTQTSSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTQTSSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Oy 61 GAGSLQHAQPPPPQPKRKPDPFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQHAQPPPPQPKRKPDPFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120  
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKGSELLKYIRKIGSPDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKGSELLKYIRKIGSPDET 180

Db 481 GPHLYYVDPVNKLKGSIPMSQSLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCCKIQ 540  
Oy 541 EVNRORYQSHPDAAVQ 556  
Db 541 EVNRORYQSHPDAAVQ 556

RESULT 3  
US-09-771-161A-245  
Sequence 245, Application US/09771161A  
Patent No. 6936450  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 803620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 245  
LENGTH: 556  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-245

Query Match 100.0%; Score 2941; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 1.4e-247;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTQTSSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTQTSSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Oy 61 GAGSLQHAQPPPPQPKRKPDPFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQHAQPPPPQPKRKPDPFKFGKILGSGSFSTVVLARELATSREYAIKILEKRII 120  
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKGSELLKYIRKIGSPDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKGSELLKYIRKIGSPDET 180  
Oy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240  
Oy 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIKLEYD 300  
Db 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIKLEYD 300  
Oy 301 FPKFPPKARDLVEKLLVLADATKRLGCEMSEGYGLKAHPFFESVTWENLHQOTPPKLT 360  
Db 301 FPKFPPKARDLVEKLLVLADATKRLGCEMSEGYGLKAHPFFESVTWENLHQOTPPKLT 360

Oy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQITDPTAKVLSPEKQARAN 240  
Oy 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIKLEYD 300  
Db 241 SFVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQKIKLEYD 300  
Oy 301 FPKFPPKARDLVEKLLVLADATKRLGCEMSEGYGLKAHPFFESVTWENLHQOTPPKLT 360  
Db 301 FPKFPPKARDLVEKLLVLADATKRLGCEMSEGYGLKAHPFFESVTWENLHQOTPPKLT 360  
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNIQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHLSASDTGLPQSGSNIQYIHDL 420  
Oy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLPARRRQLL 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQPVENNLLIOMGPVDKRGKLPARRRQLL 480  
Oy 481 GPHLYYVDPVNKLKGSIPMSQSLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCCKIQ 540  
Db 481 GPHLYYVDPVNKLKGSIPMSQSLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCCKIQ 540  
Oy 541 EVNRORYQSHPDAAVQ 556  
Db 541 EVNRORYQSHPDAAVQ 556

RESULT 5  
US-09-771-161A-154  
Sequence 154, Application US/09771161A  
Patent No. 6936450  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 803620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 154  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-154

Query Match 41.7%; Score 1227; DB 2; Length 238;  
Best Local Similarity 100.0%; Pred. No. 9.6e-99;  
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

: TELEFAX: 716-262-4113
: INFORMATION FOR SEQ ID NO: 29:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 752 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:   HYPOTHETICAL: NO
:   ANTI-SENSE: NO
:   ORIGINAL SOURCE:
:     ORGANISM: Drosophila
US-08-943-667-29

Query Match      38.9%; Score 1144.5; DB 2; Length 752;
Best Local Similarity 40.1%; Pred. No. 6.2e-91;
Matches 258; Conservative 82; Mismatches 172; Indels 131; Gaps 13;

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[illegible]

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Db      349 PSTRITQS-----LAAKGFENEDWNIANIKPVLVLAIVPATFGPSE-----TYSNIG 398
Qy
380 ----LSQPGCMQVSSSSSSHSLSASDTGLPQRSGSNIQ----YIHDLQNSPFLDLQF 430
Db      399 FVEPGLDRLAFRLANLGHIDASQSPSTFRP-----SNVEHRCDPVSSIAPIA-----N 448
Qy
431 SEDEKRL-----LEKQAGNPMQFVNNLLIKMGPDVKRGLFARRRQLLLTGPPLY 485
Db      449 SEARNRAARAQKLSEORVKNPFIPTNNSLLIKQYLEKKGGLFARRRPFLLTGPPLL 508
Qy
486 YVDPNVKVLKGEIPMSQELRPAKGFKTFVVIHTPNRTYYLMDPSGNAHMKCRKIQSVNR 545
Db      509 YIDVPHVLKGEVPTCMQVSLNKGTFPIHTPNRVYLLPDLKKADSWCKAINDV-RK 567
Qy
546 RY 547
      ||
568 RY 569

```

```

RESULT 8
US-09-205-658-159
; Sequence 159, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PstSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 632
; TYPE: CDS
; ORGANISM: Caenorhabditis elegans
US-09-205-658-159

```

```
Query Match          31.8%; Score 935; DB 2; Length 632;  
Best Local Similarity 37.2%   Pred. No. 1.1e-1072  
Matches 202; Conservative 101; Mismatches 152; Indels 88; Gaps 13;  
  
Qy      62 AGSLQHQAQPQPQRKRPRKRPDKFKPKILQEGSPGVTLARLARSFYALKIKKHKKHIIKE 121  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db      54 AKSIKEGCP-----RRTSDNMPQLSGMEGAAYSOVFRGRVATDAMPFVVLQKSYLNHR 108  
  
Qy     122 NKVPYVTRRSRRMSRLD----HPVPVKLYPTFGODESKLYPGLSYAKNGESLLKYIRKIGS 176  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db     109 ONPAIDRIEPIETLISGSCTGSSGTPGSRGPGTGGGSGGSGGSGGSGGSGGSGGSGGSGG 163
```

Qy 177 FOSTCTRTFYTABIVSALSYLHGKGIHRLDKPENILLNEDWHIQTDFGTAKVL----- 230  
Db 169 FDLMTSKTFASSIITGLQPLNDKNIHVRDMKPDNVLIQKQGHILITDPSGAQAPGGLQLS 228  
Qy 231 -----6P-----ESKQARANSFVGTAGYVSPELLTEKSACKS 262  
Db 229 QEGPTDANQASSRSSDGGSPPTFRFYGDSSESNYARRTTTPVGTALVSPMLADGDVGQV 288  
Qy 263 SDLMALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFPFKPPKARDLVEKLLVLDAT 322  
Db 289 TDIMGLGCIIPCLAGQPPFRAVNGYHLLKRIQSLDFSPPEGPPSASSIIAKILVRDPS 348  
Qy 323 KRLGCEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAYLPAHSEDDDCYGNVHL--- 379  
Db 349 TRITSQ-----LMAHKFFENVDMVNIANIKPVLHAYIPATPGEPE-----YTSNIGPV 398  
Qy 380 -----LSQFGCMQVSSSSSSSHLSASDTGLPQRSNIEQ-----YIHDLSNSFELDQ 429  
Db 399 EPGLDLRLFRLLNGLNDA-----SASQSTP-----SNVHRGDPVSEIAPRA----- 443  
Qy 430 FSEDEKRL-----LEKQAGGNPMHOFVNNLILKMGVDPKRGKLFARRRQLLSTBPHL 484  
Db 444 NSASAKNRRAARAKLESQVKNPFIPTNNSLILKQGYLKKRGKLFARRRQLLSTBPHL 503  
Qy 485 YYVDVNVKVLKGEIPWSQSLRPAKNFTKPFVHTPNRTTYLMDPSGNAHKCRKIQVSWR 544  
Db 504 LYIDVNVKVLKGEVPMTPQMVELNSQTFPIHTPNVYLLFDEKKADEWCKAINDRV 562  
Qy 545 QRY 547  
Db 563 KRY 565

RESULT 9  
US-09-538-092-216  
; Sequence 216, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurePatSeqFormatter Version 0.9  
; SEQ ID NO 216  
; LENGTH: 766  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURES:  
; NAME/KEY: misc\_feature

; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number YDR490C  
US-09-538-092-216

Query Match 24.2%; Score 712; DB 2; Length 766;  
Best Local Similarity 30.3%; Pred. No. 4.1e-53;  
Matches 187; Conservative 87; Mismatches 154; Indels 190; Gaps 15;

Qy 27 SMVRTQTSSTTPOIPQGSROG-----PAMDGT-----AASPRPQAGSLQH 67  
Db 22 SASHTQTQSYPRFPVVGSSNSQSGSELQASPOQPGSKALTSNRPIPLANDDPG---MQH 78  
Qy 68 AQP-PPORIKGRPE-----DPFKGKILGSGSFST 95  
Db 79 EMLGDPKRRRRSEMAERGAAKIVKQVDPATGELTHGVKMGIKDFKGEQLADGSSYS 138  
Qy 96 VVLARELATSREYAIIKLEKRHIIKENKVPYVTRERDVMSRLDHPFFV-KLYPTFQDEK 154  
Db 139 VVLATARDSCKYAVKVLKSKYLIHQKVKYVTVKALQKLAKTKGIFKLPTTFQDRAS 198  
Qy 155 LYFGLSYAKNGELLYKIRKISGPDSTCTRTFYTABIVSALSYLHGKGIHRLDKPENILLN 214  
Db 199 LYFLLSYAPHODFLGLIKKQYSLNSTCARYTASQIIDAVIDSLNIGIHRD:KVENILLD 258  
Qy 215 EDHIIQITDPTAKVLSPEKQ-----ARANSFVGTAGYVSPELLTEKSACKS 263  
Db 259 IQMKVKLTDFTGAKILPEPSNTADGKPYFDLYAKSKSFVGTAEYVSPPELLADNYTDSRC 318  
Qy 264 DLALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFPFKPPKARDLVEKLLVLDAT 323  
Db 319 DINAPGCILOYLAGKPPFKAANEYLTFQVKIKIQTATAGPQIVKOLVKLLVLDVND 378  
Qy 324 RLGCSEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAY-----LPAMSEDD--- 369  
Db 379 RLTIQ-----IKHLFFHEVNFEDGSVDDNPPBIQYKINAEAMKPLQKVSSEDTTV 433  
Qy 370 -----EDC 372  
Db 433 IQANLQLAGNHADTFLQAPATSQERSVISMATAAPFNKYTSOPKLGSKSTSVRSA 492  
Qy 373 YGNYDNLSPQGMQVSSSSSSSHLSASDTGLPQRSN-----IEQYIHDLSNSFELDQ 429  
Db 493 SNTDREVIOKKVSKNRASVSSPSTTSRQKNRSRSDAPWSRYLQND----- 543  
Qy 430 FSEDEKRLLEKQAG-----GNPMHOFVNNLILKMGVDPKRGKLFARRRQLLSTBPHL 469  
Db 544 -----ERVLLAKVALSTRNLEDSVGLNVALDYKNP-----LDIEPTDSAGK 588  
Qy 470 FARRRQLLSTBPHLYV 487  
Db 589 FYKQFLLITNLGRALVFV 606

RESULT 10  
US-09-248-796A-20495  
; Sequence 20495, Application US/09248796A  
; Patent No. 6747137

; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA  
ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 20495  
; LENGTH: 901  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-20495

; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; EARLIER FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 173  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Mus musculus or Homo sapiens  
US-09-205-658-173

Query Match 22.3%; Score 655.5; DB 2; Length 901;  
Best Local Similarity 37.1%; Pred. No. 4.4e-48;  
Matches 144; Conservative 69; Mismatches 116; Indels 59; Gaps 10;

Query Match 20.9%; Score 614; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 8.4e-46;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 RPGAGSLQHAQPPPO-----RKQRPEDFKFGKILGSGSFVTLARELATSREYA 109  
Db 53 QPSNRSTQOQNTSOPQOSQLAARRSARDYQPGAKIGSSTYSVALDKYTNRTYA 112  
Qy 110 IKILEKRHIIKENKVPYVTRERDVMSRL--DHPPFVKLYPTQDEKLYPGLSYAONEL 167  
Db 113 IKVLSKRHIVKENKIKYVNIKTKTLNRLGQOHGPIVQLYTFQDESSLFVLDPAHYGEL 172  
Qy 168 LKVIKIRKISGPDSTCTRTFYTABIVSALSYLHGKGIHRLDKPENILLNEDWHIQTDFGT 227  
Db 173 LSIIRKFGSLSSSVLKPFYMQIIDAIVRPIHLKGVHRLDKPENILVGHDFNLKITDPGA 232  
Qy 228 KVL-----SPE-SKQARANSFVGTAGYVSPELLTEKSACKSSDLMAL 268  
Db 233 KLLGNHSEPNQEKIDYNSVDASPEVSDTRKGSFVGTAEYVSPELLGNICOFESDIMA 292  
Qy 326 GCIIYQLVAGLPPFRAGNEYLIPOKIIKLEYDF--PEKFPKARDLVEKLLVLDATKRLG 326  
Db 293 GCILYQFFNVGPPFGKSTYLFPSKIIINVDSYKSPILPLPPOVLIQDLILSEPSARAT 352  
Qy 327 CSEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAY-----LPAMSEDDDCYGN 375  
Db 353 IPH-----IMSSRMFSDIPWDDQNPIMHRKVPFSAFGAITPSPAMPFMHUN-----OT 401  
Qy 376 YDNLSPQGMQVSSSSSSSHLSASDTG 403  
Db 402 NRNVNKSYSYTHQLQS-----QILASEG 424

Qy 263 SDLMALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFPFKPPKARDLVEKLLVLDAT 322  
Db 1 SDLMALGCIYQLVAGLPPFRAGNEYLIPOKIIKLEYDFPFKPPKARDLVEKLLVLDAT 60  
Qy 323 KRLGCEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAYLPAHSEDDDCYGN 375  
Db 61 KRLGCEMEGYGPKLKAHPFFSVTWENLHOOTPPKLTAYLPAHSEDDDCYGN 113

RESULT 12  
US-09-205-658-202  
; Sequence 202, Application US/09205658  
; Patent No. 6861256  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; EARLIER FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 202  
; LENGTH: 104  
; TYPE: PRT

RESULT 11  
US-09-205-658-173  
; Sequence 173, Application US/09205658  
; Patent No. 6861256  
; GENERAL INFORMATION:

ORGANISM: Homo sapiens  
US-09-205-656-202

Query Match 19.5%; Score 573; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2.8e-42;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 439 LEKQAGNPMQPVENNILKMGPDVDRKGLFARRRQLLLTSGPHLYYVDPVNVKLGSI 498  
Db 1 LEKQAGNPMQPVENNILKMGPDVDRKGLFARRRQLLLTSGPHLYYVDPVNVKLGSI 60

Qy 499 PWSQLRPAKNGKTFVMTNRTYYLMDPSGNAHKCRKIQEV 542  
Db 61 PWSQLRPAKNGKTFVMTNRTYYLMDPSGNAHKCRKIQEV 104

RESULT 13  
US-09-949-016-11701  
Sequence 2, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11701  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-11701

Query Match 19.4%; Score 571.5; DB 2; Length 420;  
Best Local Similarity 35.5%; Pred. No. 3e-41;  
Matches 127; Conservative 67; Mismatches 139; Indels 25; Gaps 7;

Qy 20 LCSPSPSMVIRTQTESSTPPGIPGSRQGPAMDGTAAEPKPGAGSLQHAQPPQPRKRP 79  
Db 52 LARCPQPECVKSEA-----PGLAQAAASDSRKAESTPDGAPAL---CPSPEALSPEP 103

Qy 80 -----SDPKGKILGEGSFVTVLARELATSREYAIKILEKRHIKENKVPVYTRSRDVM 134  
Db 104 PVYSIQDFTLRLVGTGTGPRVLKVKAKTAKFFALKVMSIPDVIRLKQEQHVHNSKVL 163

Qy 135 SRLDHPFFVKLYPTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDETCTRFYTAISVLS 194  
Db 164 KEVSHPLRLPMTWHDREPLVYMLAEVVPQGEISFYLRNRGRFSSITGLFYSARIICAIS 223

Query Match 19.1%; Score 562; DB 2; Length 431;  
Best Local Similarity 37.5%; Pred. No. 2.1e-40;  
Matches 123; Conservative 65; Mismatches 116; Indels 24; Gaps 7;

Qy 59 RPAAGSLQHA--QPPQPRKK-----RPEDFKPGKILGEGSFVTVLARELATS 105  
Db 62 QPQPELQANPSPPPSPSQINLQPSNPHAKPSDPHPLKVIKGSFGKVLARHKAES 121

Qy 106 REYAIKILEKRHIKENKVPVYTRSRDV-MSRLDHPFFVKLYPTFQDDEKLYFGLSYAKN 164  
Db 122 VFYAVKVLQKAILKKGEKHIKSRNVLKQVHPPFLVGLHPSPTADKLYFVLDYING 181

Qy 165 GELLKYIRKIGSFDETCTRFYTAISVLSALEYLGKGIHRLDKPENILLNEDMHQITDP 224  
Db 182 GELPYHLQRCRCFLPRARFYAAISALGYLHLSNIIVYRDLKPENILLDSQGHVITDP 241

Qy 225 GTAKVLSPEKQARANSFVGTATQVSPPELLTEKSACKSSDLWALGCIYQVLVAGLPPFRA 284  
Db 242 GLCK--ENIENHNTSTTFCQTPSYLAPEVLHKKQPYDRVTVMCLGAVLYEMLYGLPPYS 299

Qy 285 GNEYLIFOKIKLEYDFPEKFFPKARDLVKLLVLDAKRLGCEMEGYGLKHPFFES 344  
Db 300 RNTAEMVDNILNKPQLKPNHTSARHLLEGLLQKDRTKRLGAK--DDFMBSKSHVFFSL 357

Qy 345 VTWENLHQO--TPPKLTATLPAHSEDD 370  
Db 358 INMDDLINKKITPP----FNPVNSGPNR 381

RESULT 15  
US-10-000-039-2  
Sequence 2, Application US/10000039  
Patent No. 6855520  
GENERAL INFORMATION:  
APPLICANT: LANG, Florian  
WALDEGGER, Tübingen  
TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: POLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/000,039  
FILING DATE: 04-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/031,295  
FILING DATE: 26-FEB-1998

Qy 195 YLHGKGIHRLDKPENILLNEDMHQITDPGTAKVLSPEKQARANSFVGTATQVSPPELL 254  
Db 224 YLHSGKIVYRDLKPENILLDRDGHIKLTDGFAKGLVD-----RTWTLGCTPSYLAPEVI 278

Qy 255 TEKSACKSSDLWALGCIYQVLVAGLPPFRAGNEYLIFOKIIKLEYDFPEKFFPKARDLVE 314  
Db 279 QSKGHGRAVDWALGILIFSKLSGPPFPDNPFGIYQKILAGKIDFPRHLDPHVLKLIK 338

Qy 315 KLLVLDAKRLGCEMEGYGLKHPFFESVTWENLHQO--TPPKLTATLPAHSEDD 370  
Db 339 KLLVVDRTRLG-KNKGANDVQKHWPSVDEAVPQRLKPP---IVPKIGADGD 391

RESULT 14  
US-09-031-295-2  
Sequence 2, Application US/09031295  
Patent No. 6326181  
GENERAL INFORMATION:  
APPLICANT: LANG, Florian  
APPLICANT: WALDEGGER, Tübingen  
TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: POLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/031,295  
FILING DATE: 26-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 197-08-173.8  
FILING DATE: 28-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 058315/0123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-031-295-2

APPLICATION NUMBER: DE 197-08-173.8  
FILING DATE: 28-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 058315/0123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 19.1%; Score 562; DB 2; Length 431;  
Best Local Similarity 37.5%; Pred. No. 2.1e-40;  
Matches 123; Conservative 65; Mismatches 116; Indels 24; Gaps 7;

Qy 59 RPAAGSLQHA--QPPQPRKK-----RPEDFKPGKILGEGSFVTVLARELATS 105  
Db 62 QPQPELQANPSPPPSPSQINLQPSNPHAKPSDPHPLKVIKGSFGKVLARHKAES 121

Qy 106 REYAIKILEKRHIKENKVPVYTRSRDV-MSRLDHPFFVKLYPTFQDDEKLYFGLSYAKN 164  
Db 122 VFYAVKVLQKAILKKGEKHIKSRNVLKQVHPPFLVGLHPSPTADKLYFVLDYING 181

Qy 165 GELLKYIRKIGSFDETCTRFYTAISVLSALEYLGKGIHRLDKPENILLNEDMHQITDP 224  
Db 182 GELPYHLQRCRCFLPRARFYAAISALGYLHLSNIIVYRDLKPENILLDSQGHVITDP 241

Qy 225 GTAKVLSPEKQARANSFVGTATQVSPPELLTEKSACKSSDLWALGCIYQVLVAGLPPFRA 284  
Db 242 GLCK--ENIENHNTSTTFCQTPSYLAPEVLHKKQPYDRVTVMCLGAVLYEMLYGLPPYS 299

Qy 285 GNEYLIFOKIKLEYDFPEKFFPKARDLVKLLVLDAKRLGCEMEGYGLKHPFFES 344  
Db 300 RNTAEMVDNILNKPQLKPNHTSARHLLEGLLQKDRTKRLGAK--DDFMBSKSHVFFSL 357

Qy 345 VTWENLHQO--TPPKLTATLPAHSEDD 370  
Db 358 INMDDLINKKITPP----FNPVNSGPNR 381

Search completed: June 27, 2006, 01:38:02  
Job time : 53 secs

OM protein - protein search, using sw model

Run on: June 27, 2006, 01:28:03 ; Search time 298 Seconds  
(without alignments)  
1725.068 Million cell updates/sec

Title: US-10-689-576-1  
Perfect score: 2941  
Sequence: 1 MARTTSQYDAVPVIGSSVVL.....RKIGVWRQRYGSHDAAVQ 556

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2941	100.0	556	1	PDPK1_HUMAN	O15530 homo sapien
2	2941	100.0	556	2	Q6P120_HUMAN	Q6P120 homo sapien
3	2926	99.5	556	2	Q53HJ9_HUMAN	Q53HJ9 homo sapien
4	2787.5	94.8	559	1	PDPK1_RAT	O55173 rattus norv
5	2769.5	94.2	559	1	PDPK1_MOUSE	Q92280 mus musculu
6	2764.5	94.0	559	2	Q3UJZ0_MOUSE	Q3UJZ0 mus musculu
7	2758.5	93.8	559	2	Q3UKG6_MOUSE	Q3UKG6 mus musculu
8	2732.5	92.9	551	2	Q81024_MOUSE	Q81024 mus musculu
9	2626.5	89.3	532	2	Q8K1L3_MOUSE	Q8K1L3 mus musculu
10	2626.5	89.3	556	2	Q5F3U4_CHICK	Q5F3U4 gallus gall
11	2560.5	87.1	522	2	Q3TRL2_MOUSE	Q3TRL2 mus musculu
12	2391.5	81.3	558	2	Q4S4R0_TETNG	Q4S4R0 tetradodon n
13	2336	79.4	492	2	Q59EH6_HUMAN	Q59EH6 homo sapien
14	2228	75.8	537	2	Q6NZV1_BRARE	Q6NZV1 brachydanio
15	2202.5	74.9	429	2	Q9BRD5_HUMAN	Q9BRD5 homo sapien

RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).  
RX MEDLINE=98035195; PubMed=9368760; DOI=10.1016/S0960-9822(06)00336-8;  
RA Alessi D.R., Deak M., Casamayor A., Caudwell F.B., Morrice N.A.,  
RA Norman D.G., Gaffney P.R.J., Reese C.B., MacDougall C.N., Harbison D.,  
RA Ashworth A., Downes M.;  
RT "3-phosphoinositide-dependent protein kinase-1 (PDK1): structural and  
RT functional homology with the Drosophila DSTPK61 kinase.";  
RL Curr. Biol. 7:776-789(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 3).  
RC TISSUE=Myeloid;  
RX MEDLINE=98111410; PubMed=9445477; DOI=10.1126/science.279.5351.710;  
RA Stephens L.R., Anderson K.B., Stokoe D., Brdjunent-Bromage H.,  
RA Painter G.F., Holmes A.B., Gaffney P.R.J., Reese C.B., McCormick F.,  
RA Tempest P., Cozwell W.J., Hawkins P.T.;  
RT "Protein kinase B kinases that mediate phosphatidylinositol 3,4,5-  
RT trisphosphate-dependent activation of protein kinase B.";  
RL Science 279:710-714(1998).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold S.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide P.,  
RA Diatchenko L., Marusheva K., Farmer A.R., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
RA Butlerfield Y.S.W., Krzywicki M.T., Skalska U., Smilau D.E.,  
RA Schnerch A., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP MUTAGENESIS OF ARG-474, AND ALTERNATIVE SPLICING.  
RX MEDLINE=98301766; PubMed=9637919; DOI=10.1016/S0960-9822(98)70274-X;  
RA Anderson K.B., Cozwell W.J., Stephens L.R., Hawkins P.T.;  
RT "Translocation of PDK-1 to the plasma membrane is important in  
RT allowing PDK-1 to activate protein kinase B.";  
RL Curr. Biol. 8:684-691(1998).  
RN [6]  
RP PHOSPHORYLATION SITES SER-25; SER-241; SER-393; SER-396 AND SER-410,  
RP AND MUTAGENESIS OF SER-25; SER-241; SER-393; SER-396 AND SER-410.  
RX MEDLINE=99386657; PubMed=10455013; DOI=10.1042/0264-6021.3420287;  
RA Casamayor A., Morrice N.A., Alessi D.R.;  
RT "Phosphorylation of Ser-241 is essential for the activity of 3-  
RT phosphoinositide-dependent protein kinase-1: identification of five

16	2093.5	71.2	434	2	Q3UEW8_MOUSE	Q3UEW8 mus musculu
17	1933	65.7	367	2	Q9UPJ6_HUMAN	Q9UPJ6 homo sapien
18	1826	62.1	396	2	Q6A1A2_HUMAN	Q6A1A2 homo sapien
19	1710	58.1	319	2	Q9UPJ7_HUMAN	Q9UPJ7 homo sapien
20	1622.5	55.2	571	2	Q76BX2_ASTPE	Q76BX2 asterina pe
21	1431	48.7	822	2	Q9BKK6_APLCA	Q9BKK6 aplysia cal
22	1144.5	38.9	836	1	PDPK1_DROME	Q9w0v1 drosophila
23	1027	34.9	484	2	Q7PUX5_ANOGA	Q7PUX5 anopheles g
24	940	32.0	636	1	PDPK1_CABEL	Q9y1j3 caenorhabdi
25	939	31.9	813	2	Q5B8M0_EMENI	Q5B8M0 aspergillus
26	930	31.6	686	2	Q54TW2_DICDI	Q54TW2 dictyosteli
27	928	31.6	850	2	Q2UBU7_ASFPO	Q2UBU7 aspergillus
28	908.5	30.9	839	2	Q4WYD7_ASFPU	Q4WYD7 aspergillus
29	903	30.7	630	2	Q5WNC6_CABER	Q5WNC6 caenorhabdi
30	873.5	29.7	592	1	KSG1_SCHPO	Q12701 schizosacch
31	868.5	29.5	812	2	Q4HWD3_GIBZE	Q4HWD3 gibberella
32	868.5	29.5	922	2	Q873K1_NEUCR	Q873K1 neurospora
33	832.5	28.3	1542	2	Q6CFM7_YARLI	Q6CFM7 yarrowia li
34	832	28.3	488	2	Q9LZ74_ARATH	Q9LZ74 arabidopsis
35	832	28.3	491	2	Q9XFE7_ARATH	Q9XFE7 arabidopsis
36	821	27.9	498	2	Q8RUE8_ORYSA	Q8RUE8 oryza sativ
37	820	27.9	483	2	Q9SQY4_ARATH	Q9SQY4 arabidopsis
38	820	27.9	486	2	Q4VJCE_ARATH	Q4VJCE arabidopsis
39	816.5	27.8	494	2	Q516E8_LYCSB	Q516E8 lycopersico
40	800	27.2	908	2	Q54PK9_DICDI	Q54PK9 dictyosteli
41	795.5	27.0	1062	2	Q6BIK6_DESHA	Q6BIK6 debaryomyce
42	763.5	26.0	944	2	Q5A3P6_CANAL	Q5A3P6 candida alb
43	760.5	25.9	1153	2	Q5A3V9_CANAL	Q5A3V9 candida alb
44	748.5	25.5	1081	1	KOKO_YEAST	Q12236 saccharomyc
45	733	24.9	408	2	Q3B9L6_ARATH	Q3B9L6 arabidopsis

ALIGNMENTS

RESULT 1

PDPK1\_HUMAN

ID PDPK1\_HUMAN STANDARD; PRT; 556 AA.  
AC O15530;  
DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.  
DT 01-JAN-1998, sequence version 1.  
DT 07-MAR-2006, entry version 58.  
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (hPDK1).  
GN Name=PDPK1; Synonyms=PDK1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo;  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).  
RX MEDLINE=97250749; PubMed=9094314; DOI=10.1016/S0960-9822(06)00122-0;  
RA Alessi D.R., James S.R., Downes C.P., Holmes A.B., Gaffney P.R.J.,  
RA Reese C.B., Cohen P.;  
RT "Characterization of a 3-phosphoinositide-dependent protein kinase  
RT which phosphorylates and activates protein kinase B alpha.";  
RL Curr. Biol. 7:261-269(1997).

RT sites of phosphorylation in vivo.";  
RL Biochem. J. 342:287-292(1999).  
RN [7]  
RP MUTAGENESIS OF ALA-277.  
RX MEDLINE=99392684; PubMed=10364160;  
RA Paradis E., Allion M., Toker A., Thomas J.H., Ruvkun G.;  
RT "A PDK1 homolog is necessary and sufficient to transduce AGE-1 PI3  
RT kinase signals that regulate diapause in *Caenorhabditis elegans*.";  
RL Genes Dev. 13:1438-1452(1999).  
RN [8]  
RP PHOSPHORYLATION SITES TYR-9; SER-241; TYR-373 AND TYR-376, AND  
RP MUTAGENESIS OF TYR-9; TYR-373 AND TYR-376.  
RX MEDLINE=21463095; PubMed=11481331; DOI=10.1074/jbc.M105916200;  
RA Park J., Hill M.M., Hess D., Brazil D.P., Hofsteenge J.,  
RA Hemmings B.A.;  
RT "Identification of tyrosine phosphorylation sites on 3-  
RT phosphoinositide-dependent protein kinase-1 (PDK1) and their role in  
RT regulating kinase activity.";  
RL J. Biol. Chem. 276:37459-37471(2001).  
RN [9]  
RP PHOSPHORYLATION SITE SER-241.  
RX PubMed=15302935; DOI=10.1073/pnas.0404720101;  
RA Beaulieu S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,  
RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;  
RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).  
CC -1- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also  
CC PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in  
CC signaling processes and in development (By similarity). Isoform 3  
CC is catalytically inactive.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after  
CC cell stimulation leading to its translocation. Tyrosine  
CC phosphorylation seems to occur only at the plasma membrane.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1;  
CC IsoId=O15530-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=O15530-2; Sequence=VSP\_004894;  
CC Name=3;  
CC IsoId=O15530-3; Sequence=VSP\_004895;  
CC -1- TISSUE SPECIFICITY: Appears to be expressed ubiquitously.  
CC -1- PTM: Phosphorylated on tyrosine and serine/threonine.  
CC Phosphorylation on Ser-241 in the activation loop is required for  
CC full activity. PDK1 itself can autophosphorylate Ser-241, leading  
CC to its own activation.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1  
CC subfamily.  
CC -1- SIMILARITY: Contains 1 PH domain.  
CC .....  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC .....  
DR EMBL; AF017995; AAC51825.1; -; mRNA.  
DR EMBL; Y15056; CAA75341.1; -; mRNA.  
DR EMBL; BC012103; AAH12103.1; -; mRNA.

DR PDB: 1H1W; X-ray; A=71-359.  
DR PDB: 1OKY; X-ray; A=51-360.  
DR PDB: 1OKY; X-ray; A=51-360.  
DR PDB: 1UJ3; X-ray; A=51-360.  
DR PDB: 1UJ7; X-ray; A=51-360.  
DR PDB: 1UJ8; X-ray; A=51-360.  
DR PDB: 1UJ9; X-ray; A=72-357.  
DR PDB: 1UVR; X-ray; A=71-359.  
DR PDB: 1W1D; X-ray; A=409-556.  
DR PDB: 1W1Q; X-ray; A=409-556.  
DR PDB: 1W1H; X-ray; A/B/C/D=409-556.  
DR PDB: 1Z5M; X-ray; A=74-359.  
DR PDB: 2B1Y; X-ray; A=51-360.  
DR Ensembl: ENSG00000140992; Homo sapiens.  
DR H-invDB: HIX0012732; .  
DR HGNC: HGNC:6816; PDPK1.  
DR MIM: 605213; gene.  
DR LinkHub: O15530; .  
DR GO: GO:0005737; C:cytoplasm; ISP.  
DR GO: GO:0005886; C:plasma membrane; ISP.  
DR GO: GO:0004676; P:3-phosphoinositide-dependent protein kinase. . .; TAS.  
DR GO: GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.  
DR GO: GO:0008286; P:insulin receptor signaling pathway; TAS.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.  
DR InterPro: IPR01849; PH.  
DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR022290; Ser\_thr\_pkinase.  
DR InterPro: IPR01245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00003; PH\_DOMAIN; FALSE NEG.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW 3D-structure; Alternative splicing; ATP-binding; Kinase; Membrane;  
KW Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;  
KW Transferase.  
FT CHAIN 1 556 3-phosphoinositide-dependent protein  
FT kinase 1.  
FT /FTID=PRO\_0000086500.  
FT DOMAIN 82 342 Protein kinase.  
FT NP\_BIND 459 550 PH.  
FT COMPBIAS 389 398 ATP (By similarity).  
FT ACT\_SITE 205 205 Proton acceptor (By similarity).  
FT BINDING 111 111 ATP (By similarity).  
FT MOD\_RES 9 9 Phosphotyrosine.  
FT MOD\_RES 25 25 Phosphoserine.  
FT MOD\_RES 241 241 Phosphoserine (by autocatalysis).  
FT MOD\_RES 373 373 Phosphotyrosine.  
FT MOD\_RES 376 376 Phosphotyrosine.  
FT MOD\_RES 393 393 Phosphoserine.  
FT MOD\_RES 396 396 Phosphoserine.  
FT MOD\_RES 410 410 Phosphoserine.

FT VARSPLIC 1 50 Missing (in isoform 2).  
FT VARSPLIC 238 263 /FTID=VSP\_004894.  
FT VARSPLIC 238 263 Missing (in isoform 3).  
FT MUTAGEN 9 9 Y->F: Slight reduction in pervanadate-  
FT MUTAGEN 25 25 stimulated tyrosine phosphorylation.  
FT MUTAGEN 241 241 S->A: No effect.  
FT MUTAGEN 277 277 S->A: No activation.  
FT A->V: 3-fold increase in kinase activity.

Query Match 100.0%; Score 2941; DB 1; Length 556;  
Best Local Similarity 100.0%; Pred. No. 3.5e-184;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSTPPGIPGSGRQGPAMDGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSTPPGIPGSGRQGPAMDGTAAEPRP 60  
Oy 61 GAGSLQAQPPPPQPKRQPEDPKFGKILGSGSPSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQAQPPPPQPKRQPEDPKFGKILGSGSPSTVVLARELATSREYAIKILEKRII 120  
Oy 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180  
Oy 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQITDPTGAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQITDPTGAKVLSPEKQARAN 240  
Oy 241 SPVGTAAQYVPELLTEKSACKSSDLNALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300  
Db 241 SPVGTAAQYVPELLTEKSACKSSDLNALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300  
Oy 301 FPEKFPFKARDLVEKLLVLADATKRLGCESEMGYGLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 FPEKFPFKARDLVEKLLVLADATKRLGCESEMGYGLKAHPFESVTWENLHQOTPPKLT 360  
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIQYIHDL 420  
Oy 421 SNSFELDQFSEDEKRLLEKQAGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480  
Oy 481 GHLYYVDPVNKLKGIIPWSQLPEAAGNFTFVHTPTRTTYLADPSNAHKMKRQ 540  
Db 481 GHLYYVDPVNKLKGIIPWSQLPEAAGNFTFVHTPTRTTYLADPSNAHKMKRQ 540  
Oy 541 EVNRORYOSHDAAVQ 556  
Db 541 EVNRORYOSHDAAVQ 556

RESULT 2  
Q6FI20\_HUMAN

ID Q6FI20\_HUMAN PRELIMINARY; PRT; 556 AA.  
AC Q6FI20;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 21-FEB-2006, entry version 10.  
DE PDPK1 protein.  
GN Name=PDPK1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,  
RA Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., LeBeur J.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein + ADP + a phosphoprotein.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL: CR536517; CAG38755.1; -; mRNA.  
DR SMR: Q6FI20; 72-358, 409-556.  
DR Ensembl: ENSG00000140992; Homo sapiens.  
DR GO: GO:0005524; P:ATP binding; IEA.  
DR GO: GO:0000166; F:nucleotide binding; IEA.  
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; P:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR022290; Ser\_thr\_pkinase.  
DR InterPro: IPR01245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 556 AA; 63152 MW; EDBC0306DC4D0653 CRC64;

Query Match 100.0%; Score 2941; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 3.5e-184;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSTPPGIPGSGRQGPAMDGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTSSTPPGIPGSGRQGPAMDGTAAEPRP 60  
Oy 61 GAGSLQAQPPPPQPKRQPEDPKFGKILGSGSPSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQAQPPPPQPKRQPEDPKFGKILGSGSPSTVVLARELATSREYAIKILEKRII 120

Oy 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMRLDHPFFVKLYFTPDDEKLYFGLSYAKGKLLKYIRKIGSFDET 180  
Oy 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQITDPTGAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPEINILLNEDMHQITDPTGAKVLSPEKQARAN 240  
Oy 241 SPVGTAAQYVPELLTEKSACKSSDLNALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300  
Db 241 SPVGTAAQYVPELLTEKSACKSSDLNALGCIYQLVAGLPPFRAGNEYLIFOKIKLEYD 300  
Oy 301 FPEKFPFKARDLVEKLLVLADATKRLGCESEMGYGLKAHPFESVTWENLHQOTPPKLT 360  
Db 301 FPEKFPFKARDLVEKLLVLADATKRLGCESEMGYGLKAHPFESVTWENLHQOTPPKLT 360  
Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSHSLASDTGLPQSGSNIQYIHDL 420  
Oy 421 SNSFELDQFSEDEKRLLEKQAGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGNPMHQPVENNLILOMGPDVKRGLFARRRQLL 480  
Oy 481 GHLYYVDPVNKLKGIIPWSQLPEAAGNFTFVHTPTRTTYLADPSNAHKMKRQ 540  
Db 481 GHLYYVDPVNKLKGIIPWSQLPEAAGNFTFVHTPTRTTYLADPSNAHKMKRQ 540  
Oy 541 EVNRORYOSHDAAVQ 556  
Db 541 EVNRORYOSHDAAVQ 556

RESULT 3  
Q53HJ9\_HUMAN  
ID Q53HJ9\_HUMAN PRELIMINARY; PRT; 556 AA.  
AC Q53HJ9;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 6.  
DR 3-phosphoinositide dependent protein kinase-1 variant (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Coronary artery;  
RC MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;  
RA Maruyama K., Sugano S.;  
RT "Oligo-capping: a simple method to replace the cap structure of  
eucaryotic mRNAs with oligoribonucleotides.";  
RL Gene 138:171-174(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Coronary artery;  
RX MEDLINE=9803886; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;  
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.,  
RT "Construction and characterization of a full length-enriched and a 5'-  
end-enriched cDNA library.";  
RL Gene 200:149-156(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Coronary artery;  
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,  
Tanaka A., Yokoyama S.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC .....  
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC .....  
DR EMBL: AJ222581; BAD96301.1; -; mRNA.  
DR SMR: Q53HJ9; 72-358, 409-556.  
DR Ensembl: ENSG00000104992; Homo sapiens.  
DR GO: GO:0005524; P:ATP binding; IEA.  
DR GO: GO:0000166; P:nucleotide binding; IEA.  
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; P:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Kinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
FT NON\_TER 1 1  
SQ SEQUENCE 556 AA; 63126 MW; B8ED4F687C7D958C CRC64;

Query Match 99.5%; Score 2926; DB 2; Length 556;  
Best Local Similarity 99.5%; Pred. No. 3.4e-183;  
Matches 553; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Oy 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRIK 120  
Db 61 GAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRIK 120  
Oy 121 ENKVPYVTRERDVMSRLDHPFVKLYPTFQDDEKLYFGLSYAKNGELLYKIRKIGSF 180  
Db 121 ENKVPYVTRERDVMSRLDHPFVKLYPTFQDDEKLYFGLSYAKNGELLYKIRKIGSF 180

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after  
cell stimulation leading to its translocation. Tyrosine  
phosphorylation seems to occur only at the plasma membrane (By  
similarity).  
CC -1- PTM: Phosphorylated on tyrosine and serine/threonine.  
CC Phosphorylation on Ser-244 in the activation loop is required for  
full activity. PDK1 itself can autophosphorylate Ser-244, leading  
to its own activation (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1  
subfamily.  
CC -1- SIMILARITY: Contains 1 PH domain.  
CC .....  
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC .....  
DR EMBL: Y15748; CAA75758.1; -; mRNA.  
DR HSP: Q15530; 1H1W.  
DR SMR: Q55173; 75-361, 412-559.  
DR Ensembl: ENSRNOG0000006136; Rattus norvegicus.  
DR RGD: 620307; Pdk1.  
DR InterPro: IPR001849; PH.  
DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Kinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PH\_DOMAIN; FALSE\_NEG.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Membrane; Nucleotide-binding; Phosphorylation;  
KW Serine/threonine-protein kinase; Transferase.  
FT CHAIN 1 559 3-phosphoinositide-dependent protein  
FT kinase 1.  
FT FTID=PRO\_0000086502.  
FT Protein kinase.  
FT DOMAIN 85 345 PH.  
FT NP\_BIND 91 99 ATP (By similarity).  
FT COMPBIAS 392 399 Poly-Ser.  
FT ACT\_SITE 208 208 Proton acceptor (By similarity).  
FT BINDING 114 114 ATP (By similarity).  
FT MOD\_RES 9 9 Phosphotyrosine (By similarity).  
FT MOD\_RES 25 25 Phosphoserine (By similarity).  
FT MOD\_RES 244 244 Phosphoserine (By autocatalysis) (By  
FT similarity).  
FT MOD\_RES 376 376 Phosphotyrosine (By similarity).  
FT MOD\_RES 379 379 Phosphotyrosine (By similarity).  
FT MOD\_RES 396 396 Phosphoserine (By similarity).  
FT MOD\_RES 399 399 Phosphoserine (By similarity).  
FT MOD\_RES 406 406 Phosphoserine (By similarity).  
FT MOD\_RES 413 413 Phosphoserine (By similarity).  
SQ SEQUENCE 559 AA; 63609 MW; ADR70A7F6C2A20BF CRC64;

Oy 181 CTRPTTABIIVSALEYLHGKGIHRDLKPEINLLNEDMHQIOTDPTAKVLSPEKQARAN 240  
Db 181 CTRPTTABIIVSALEYLHGKGIHRDLKPEINLLNEDMHQIOTDPTAKVLSPEKQARAN 240  
Oy 241 SPVGTAGVYSPPELLTEKSACKSSDLWALGCIYQVAVGLPFPFRAGNEYLIPOKIILKLYD 300  
Db 241 SPVGTAGVYSPPELLTEKSACKSSDLWALGCIYQVAVGLPFPFRAGNEYLIPOKIILKLYD 300  
Oy 301 FPEKFPFKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQQTTPPKLTA 360  
Db 301 FPEKFPFKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQQTTPPKLTA 360  
Oy 361 YLPAMSEDEDEDYGYNDNLSPGQCHVSSSSSSSLASDTGLPQRSGSNIQYIHLHD 420  
Db 361 YLPAMSEDEDEDYGYNDNLSPGQCHVSSSSSSSLASDTGLPQRSGSNIQYIHLHD 420  
Oy 421 SNSFELDLPQSFSEDKRLLEKQAGGNPHQFVNNLLIQGPPVDKRGFLFARRRQLL 480  
Db 421 SNSFELDLPQSFSEDKRLLEKQAGGNPHQFVNNLLIQGPPVDKRGFLFARRRQLL 480  
Oy 481 GPHLYYVDVNVKVLKGIIPWSQSLRPEAKNFKTFPVHTPNRTYYLMDPSNAHKWCRKI 540  
Db 481 GPHLYYVDVNVKVLKGIIPWSQSLRPEAKNFKTFPVHTPNRTYYLMDPSNAHKWCRKI 540  
Oy 541 EVMQRQYQSHPDAAVQ 556  
Db 541 EVMQRQYQSHPDAAVQ 556

RESULT 4  
PDPK1\_RAT  
ID PDPK1\_RAT STANDARD; PRT; 559 AA.  
AC O55173;  
DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-1998, sequence version 1.  
DT 07-MAR-2006, entry version 42.  
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (Protein  
kinase B kinase) (PKB kinase).  
GN Name=Pdk1; Synonyms=Pdk1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=98111410; PubMed=9445477; DOI=10.1126/science.279.5351.710;  
RA Stephens L.R., Anderson K.E., Skokos D., Erdjument-Bromage H.,  
RA Painter G.P., Holmes A.B., Gaffney P.R.J., Reese C.B., McCormick F.,  
RA Tempest P., Coadwell W.J., Hawkins P.T.;  
RT "Protein kinase B kinases that mediate phosphatidylinositol 3,4,5-  
trisphosphate-dependent activation of protein kinase B.";  
RL Science 279:710-714(1998).  
CC -1- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also  
CC PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in  
CC signaling processes and in development (By similarity).  
CC

Query Match 94.8%; Score 2787.5; DB 1; Length 559;  
Best Local Similarity 95.2%; Pred. No. 4.1e-174;  
Matches 532; Conservative 6; Mismatches 18; Indels 3; Gaps 2;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 59  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 60  
Oy 60 PGAGSLQHAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRIK 117  
Db 61 PSTNPLQGHQAQPPQPRKGRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILKRIK 120  
Oy 118 IIKENKVPYVTRERDVMSRLDHPFVKLYPTFQDDEKLYFGLSYAKNGELLYKIRKIGSF 177  
Db 121 IIKENKVPYVTRERDVMSRLDHPFVKLYPTFQDDEKLYFGLSYAKNGELLYKIRKIGSF 180  
Oy 178 DDTCTRTFTABIIVSALEYLHGKGIHRDLKPEINLLNEDMHQIOTDPTAKVLSPEKQ 237  
Db 181 DDTCTRTFTABIIVSALEYLHGKGIHRDLKPEINLLNEDMHQIOTDPTAKVLSPEKQ 240  
Oy 238 RANSFVGTAGVYSPPELLTEKSACKSSDLWALGCIYQVAVGLPFPFRAGNEYLIPOKIILK 297  
Db 241 RANSFVGTAGVYSPPELLTEKSACKSSDLWALGCIYQVAVGLPFPFRAGNEYLIPOKIILK 300  
Oy 298 EYDFPEKFPFKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQQTTPPK 357  
Db 301 EYDFPEKFPFKARDLVEKLLVLDATKRLGCESEMGYGLKAHPFFESVTWENLHQQTTPPK 360  
Oy 358 LTAYLPAMSEDEDEDYGYNDNLSPGQCHVSSSSSSSLASDTGLPQRSGSNIQYIHL 417  
Db 361 LTAYLPAMSEDEDEDYGYNDNLSPGQCHVSSSSSSSLASDTGLPQRSGSNIQYIHL 420  
Oy 418 DLDNSFELDLPQSFSEDKRLLEKQAGGNPHQFVNNLLIQGPPVDKRGFLFARRRQL 477  
Db 421 DLDNSFELDLPQSFSEDKRLLEKQAGGNPHQFVNNLLIQGPPVDKRGFLFARRRQL 480  
Oy 478 LTGPHLYYVDVNVKVLKGIIPWSQSLRPEAKNFKTFPVHTPNRTYYLMDPSNAHKWCR 537  
Db 481 LTGPHLYYVDVNVKVLKGIIPWSQSLRPEAKNFKTFPVHTPNRTYYLMDPSNAHKWCR 540  
Oy 538 KIQBWRQYQSHPDAAVQ 556  
Db 541 KIQBWRQYQSHPDAAVQ 559

RESULT 5  
PDK1\_MOUSE  
ID PDK1\_MOUSE STANDARD; PRT; 559 AA.  
AC Q9Z2A0; Q9R1D8; Q9R215;  
DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.  
DT 18-OCT-2001, sequence version 2.  
DT 07-MAR-2006, entry version 44.  
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (mPDK1).  
GN Name=Pdk1; Synonyms=Pdk1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID:10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Liver;  
RX MEDLINE=99175193; PubMed=10075713; DOI=10.1074/jbc.274.12.8117;  
RA Dong L.Q., Zhang R.-B., Langlaie P., He H., Clark M., Zhu L., Liu F.;  
RT "Primary structure, tissue distribution, and expression of mouse  
phosphoinositide-dependent protein kinase-1, a protein kinase that  
phosphorylates and activates protein kinase C zeta.";  
RL J. Biol. Chem. 274:8117-8122(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Brain;  
RA Park J., Hemmings B.A.;  
RT "Mouse phosphoinositide-dependent protein kinase 1 (mPDK1).";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC STRAIN=C57BL/6;  
RA Xu P., Taylor S.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also  
PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in  
signaling processes and in development. Could also play a role in  
sex differentiation processes.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after  
cell stimulation leading to its translocation. Tyrosine  
phosphorylation seems to occur only at the plasma membrane.  
CC -1- TISSUE SPECIFICITY: Highly expressed in heart, brain, liver and  
testis, also expressed in embryonic cells.  
CC -1- PTM: Phosphorylated on tyrosine and serine/threonine.  
CC Phosphorylation on Ser-244 in the activation loop is required for  
full activity. PDK1 itself can autophosphorylate Ser-244, leading  
to its own activation (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1  
subfamily.  
CC -1- SIMILARITY: Contains 1 PH domain.  
CC -----  
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL: AF086625; AAC67544.1; -. mRNA.  
DR EMBL: AF126294; AAD38505.1; -. mRNA.  
DR EMBL: AF079535; AAC96115.1; -. mRNA.  
DR HSP: O15530; 1H1M.  
DR SMR: Q922A0; 75-361, 412-559.  
DR InAct: Q922A0; -.  
DR Ensembl: ENSMUSG0000024122; Mus musculus.  
DR MGI: MGI:1338068; Pdk1.  
DR GO: GO:0005737; C:cytoplasm; IDA.  
DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.  
DR GO: GO:0004676; F:3-phosphoinositide-dependent protein kinase. .; IDA.  
DR GO: GO:0006972; P:hyperosmotic response; IDA.  
DR GO: GO:0007165; P:signal transduction; TAS.  
DR InterPro: IPR001849; PH.

DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_Kinase.  
DR InterPro: IPR008271; Ser\_thr\_kin\_A5.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00003; PH\_DOMAIN; FALSE\_NEG.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Membrane; Nucleotide-binding; Phosphorylation;  
Serine/threonine-protein kinase; Transferase.  
KW CHAIN 1 559 3-phosphoinositide-dependent protein  
kinase 1  
FT /FTID:PRO\_0000086501.  
FT Protein Kinase.  
FT DOMAIN 85 345  
FT NP\_BIND 462 553  
FT ACT\_SITE 91 99 ATP (By similarity).  
FT COMPBIAS 392 401 Poly-Ser.  
FT BINDING 208 208 Protein acceptor (By similarity).  
FT MOD\_RES 114 114 ATP (By similarity).  
FT MOD\_RES 9 9 Phosphotyrosine (By similarity).  
FT MOD\_RES 25 25 Phosphoserine (By similarity).  
FT MOD\_RES 244 244 Phosphoserine (by autocatalysis) (By  
similarity).  
FT MOD\_RES 376 376 Phosphotyrosine (By similarity).  
FT MOD\_RES 379 379 Phosphotyrosine (By similarity).  
FT MOD\_RES 396 396 Phosphoserine (By similarity).  
FT MOD\_RES 399 399 Phosphoserine (By similarity).  
FT MOD\_RES 406 406 Phosphoserine (By similarity).  
FT MOD\_RES 413 413 Phosphoserine (By similarity).  
FT CONFLICT 84 84 D -> N (in Ref. 1).  
FT CONFLICT 248 248 T -> P (in Ref. 3).  
FT CONFLICT 285 285 F -> S (in Ref. 3).  
FT CONFLICT 546 546 W -> R (in Ref. 3).  
SQ SEQUENCE 559 AA; 63759 MW; 27460FAC9 CRC64;

Query Match 94.24; Score 2769.5; DB 1; Length 559;  
Best Local Similarity 94.6%; Pred. No. 6.2a-173;  
Matches 529; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

Oy 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTSSTPGIIPGG-SROGPAQMDTAEPK 59  
Db 1 MARTTSQLYDAVPIQSSVVLCSGSPSMVTRTSSTPGIIPGG-SROGPAQMDTAEPK 60  
Oy 60 PGAGSLQH-AQPPQPKRKRDPKPKGLGSGSFTVVLRLSLATSRBYAIKILKRX 117  
Db 61 PSTNPLQGHPAQLPPQPKRKRDPKPKGLGSGSFTVVLRLSLATSRBYAIKILKRX 120  
Oy 118 IIKENKVPVYTRERDVMRLHDPFFVLYVTFQDDSKLYFGLSYAKNELLKYIRKIGSF 177  
Db 121 IIKENKVPVYTRERDVMRLHDPFFVLYVTFQDDSKLYFGLSYAKNELLKYIRKIGSF 180  
Oy 178 DETCTRYTARIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDFGTAKVLSPEKQA 237

Db 181 DETCTRYTARIVSALSYLHGKGIHRLDKPENILLNEDMHIQITDFGTAKVLSPEKQA 240  
Oy 238 RANSPVGTATQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPFRAGNEVLIPOKIIL 297  
Db 241 RANSPVGTATQVSPPELLTEKSACKSSDLWALGCIYQLVAGLPFRAGNEVLIPOKIIL 300  
Oy 298 EYDPPEKFFPKARDLVSKLLVLDATKRLGCSKSGYGLKXHPFBSVWNLHQOTPPK 357  
Db 301 EYHPPKFFPKARDLVSKLLVLDATKRLGCSKSGYGLKXHPFBSVWNLHQOTPPK 360  
Oy 358 LTATYLPAMSEDDDCYGNVDNLLSGFGCHQVSSSSSSHSLSASDTGLPQSGNSIYOYIH 417  
Db 361 LTATYLPAMSEDDDCYGNVDNLLSGFGCHQVSSSSSSHSLSASDTGLPQSGNSIYOYIH 420  
Oy 418 DLDSNSFELDQFSEDEKRLLEKAGGNPMHQPVENNLIQMGVVDKRLGLFARRRQLL 477  
Db 421 DLDTNSFELDQFSEDEKRLLEKAGGNPMHQPVENNLIQMGVVDKRLGLFARRRQLL 480  
Oy 478 LTGPHLYYVDPVNVKLGKSPMSQLRPAKNKTFPVHTNRTTYLMDPSGNHAKWCR 537  
Db 481 LTGPHLYYVDPVNVKLGKSPMSQLRPAKNKTFPVHTNRTTYLMDPSGNHAKWCR 540  
Oy 538 KIOEVNRQRYQSHPDAAVQ 556  
Db 541 KIOEVNRQRYQSHPDAAVQ 559

RESULT 6  
QJUNZO MOUSE  
ID QJUNZO\_MOUSE PRELIMINARY; PRT; 559 AA.  
AC QJUNZO;  
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
DT 11-OCT-2005, sequence version 1.  
DT 21-FEB-2006, entry version 8.  
DE CDNA, RIKEN full-length enriched library, clone:192018K11 product:3-  
DE phosphoinositide dependent protein kinase-1, full insert sequence.  
GN Name=Pdk1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID:10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-4;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 203:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
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RL Science 309:1559-1563(2005).  
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RP NUCLEOTIDE SEQUENCE.  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
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RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
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 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
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 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
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 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
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RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
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 Muramatsu M., Hayashizaki Y.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein + ADP + a phosphoprotein.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC .....  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC .....  
 DR EMBL: AK147149; BAB27716.1; -; mRNA.  
 DR MGI: MGI:1338068; Pdpk1.  
 DR GO: GO:0005737; C:cytoplasm; IDA.  
 DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.  
 DR GO: GO:004676; P:3-phosphoinositide-dependent protein kinase. . .; IDA.  
 DR GO: GO:0006972; P:hyperosmotic response; IDA.  
 DR GO: GO:0007165; P:signal transduction; TAS.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR008271; Ser\_thr\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KM ATP-binding; Kinase; Nucleotide-binding;  
 KM Serine/threonine-protein kinase; Transferrase.  
 SQ SEQUENCE 559 AA; 63729 MW; F0D6AED27161F6B8 CRC64;

Query Match 94.0%; Score 2764.5; DB 2; Length 559;  
 Best Local Similarity 94.5%; Pred. No. 1,3e-172;  
 Matches 528; Conservative 8; Mismatches 20; Indels 3; Gaps 2;  
 QY 1 MARTTSQLYDAVPIQSSVVLCSFSPMSVTRTSTSPGPGG-SROGPMQDGTAAAPR 59  
 DB 1 MARTTSQLYDAVPIQSSVVLCSFSPMSVTRTSTSPGPGG-SROGPMQDGTAAAPR 60  
 QY 60 PQAGSLQH-AAQPPQPKRKPDPFKPKILGEGSFSTVVLARSLSRYAIAKILKRXH 117  
 DB 61 PSTNPLQHQPAQLPQPKRKPDPFKPKILGEGSFSTVVLARSLSRYAIAKILKRXH 120  
 QY 118 IIKENKVPVYTRERDVMRLHPPFVLYVTFPDDSKLYFGLSYAKNGELLKYIKIGSF 177  
 DB 121 IIKENKVPVYTRERDVMRLHPPFVLYVTFPDDSKLYFGLSYAKNGELLKYIKIGSF 180  
 QY 178 DETCTPYTARISVALEYLHGKGIHRLDKPENILLNEDMHQITQDFTAKVLSPEKQA 237  
 DB 181 DEACTPYTARISVALEYLHGKGIHRLDKPENILLNEDMHQITQDFTAKVLSPEKQA 240

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 DB 241 RANSFVGTQAVSPPELLTSKSSDMLAGCIIYQLVAGLPFRAGNEYLIFQKIIKL 300  
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 DB 301 EYDFPEKFPKARDLVSKLLVLDATKRLGCEMGYGLKAPHPFSSVTWENLHQOTPPK 360  
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 DB 421 DLOSNSFELDQLFSSDEKRLLEKQAQGNPHQVFNENLILKMGVVDKRGKLFARRQLL 480  
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 QY 538 KIQEVNRQRYQSHPDAAVQ 556  
 DB 541 KIQEVNRQRYQSHPDAAVQ 559

RESULT 7  
 Q3UK6 MOUSE  
 ID Q3UK6\_MOUSE PRELIMINARY; PRT; 559 AA.  
 AC Q3UK6;  
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
 DT 11-OCT-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 8.  
 DE Melanocyte cDNA, RIKEN full-length enriched library, clone:G270062J02  
 DE product:3-phosphoinositide dependent protein kinase-1, full insert  
 DE sequence.  
 GN Name=Pdpk1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
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RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RA Arawaka T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
Shibata K., Shireki T., Tagami M., Tagami Y., Waki K., Watahiki A.,  
Muramatsu M., Hayashizaki Y.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL: AK147835; BAE28171.1; -; mRNA.  
DR MGI: MGI:1338068; Pdpk1.  
DR GO: GO:0005737; C:cytoplasm; IDA.  
DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.  
DR GO: GO:0004676; P:3-phosphoinositide-dependent protein kinase. . .; IDA.  
DR GO: GO:0006972; P:hyperosmotic response; IDA.  
DR GO: GO:0007165; P:signal transduction; TAS.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR ATP-binding; Kinase; Nucleotide-binding;  
DR Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 559 AA; 63687 MW; 74461D027460FAC6 CRC64;

Query Match 93.8%; Score 2758.5; DB 2; Length 559;  
Best Local Similarity 94.3%; Pred. No. 3.3e-172;  
Matches 527; Conservative 9; Mismatches 20; Indels 3; Gaps 2;

Qy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRVTQTESSTPPGPG-SRQGPAMDGTAAEPR 59  
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRVTQTESSTPPGPG-SRQGPAMDGTAAEPR 60  
Qy 60 PGAGSLQH--AQQPPQPKRQRPEDFKFGKILGSGSFSTVLLARSLATSRYAIIKILSKRH 117  
Db 61 PSTNPLOQHPAQLPQPKRQRPEDFKFGKILGSGSFSTVLLARSLATSRYAIIKILSKRH 120

Qy 118 I I K E N K V P Y T R E D V M S R L O H P F V K L Y T F Q D E K L Y P G L S Y A K G E L L Y I R K I G S F 177  
Db 121 I I K E N K V P Y T R E D V M S R L O H P F V K L Y T F Q D E K L Y P G L S Y A K G E L L Y I R K I G S F 180  
Qy 178 D E T C T R F T T A S I V S A L E Y L G K G I I H R D L K P E N I L L N E D M H I Q I T D P G T A K V L S P E S K Q A 237  
Db 181 D E T C T R F T T A S I V S A L E Y L G K G I I H R D L K P E N I L L N E D M H I Q I T D P G T A K V L S P E S K Q A 240  
Qy 238 R A N S F V G T A Q V S P E L L T E K S A C K S S D L M A L G C I I Y Q L V A G L P P F R A G N E Y L I P Q K I I K L 297  
Db 241 R A N S F V G T A Q V S P E L L T E K S A C K S S D L M A L G C I I Y Q L V A G L P P F R A G N E Y L I P Q K I I K L 300  
Qy 298 E Y D F P E K F F P K A R D L V E K L L V D A T K R L G C E M E G Y P L K A H P F F S V T W N L H Q O T P P K 357  
Db 301 E Y H F P E K F F P K A R D L V E K L L V D A T K R L G C E M E G Y P L K A H P F F T I T W N L H Q O T P P K 360  
Qy 358 L T A V L P A M S E D D E D C Y G N Y D N L S Q P G F M Q V S S S S S H S L S A S D T G L P O R S G S N I E Q Y I H 417  
Db 361 L T A V L P A M S E D D E D C Y G N Y D N L S Q P G F M Q V S S S S S H S L S A S D T G L P O R S G S N I E Q Y I H 420  
Qy 418 D L D S N S F E L D Q F S E D K R L L L K Q A G N P W H Q F V E N L I L K G P V D K R K G L F A R R Q L L 477  
Db 421 D L D T N S F E L D Q F S E D K R L L L K Q A G N P W H Q F V E N L I L K G P V D K R K G L F A R R Q L L 480  
Qy 478 L T E G P H L Y Y D P V N K V L K G E I P M S Q S L R P E A N F K T F P V H T P A R T Y Y L A D P S N A H K M C R 537  
Db 481 L T E G P H L Y Y D P V N K V L K G E I P M S Q S L R P E A N F K T F P V H T P A R T Y Y L A D P S N A H K M C R 540  
Qy 538 K I Q G V R Q Y Q S H P D A A V 556  
Db 541 K I Q G V R Q Y Q S H P D A A V 559

RESULT 8  
Q81024\_MOUSE  
ID Q81024\_MOUSE PRELIMINARY; PRT; 551 AA.  
AC Q81024;  
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2003, sequence version 1.  
DT 07-FEB-2006, entry version 15.  
DE PDK1 (Fragment).  
GN Name=Pdpk1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
RN NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SvJ;  
RA Brathwaite M., Waelts P., Schlessinger D., Nagaraja R.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----  
DR EMBL: AY162410; AA017164.1; -; Genomic DNA.  
DR HSP: Q15530; ILM.  
DR SRR: Q81024; 67-353, 404-551.  
DR Ensembl: ENSMUSG00000024122; Mus musculus.  
DR GO: GO:0005524; P:ATP binding; IEA.  
DR GO: GO:0000166; P:nucleotide binding; IEA.  
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; P:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR ATP-binding; Kinase; Nucleotide-binding;  
DR Serine/threonine-protein kinase; Transferase.  
FT NON\_TER 1 1  
SQ SEQUENCE 551 AA; 62870 MW; ACC31D51439282F4 CRC64;

Query Match 92.9%; Score 2732.5; DB 2; Length 551;  
Best Local Similarity 94.6%; Pred. No. 1.6e-170;  
Matches 521; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

Qy 9 YDAVPIQSSVVLSCSPSPMVRVTQTESSTPPGPG-SRQGPAMDGTAAEPRPGAGSLQH 67  
Db 1 YDAVPIQSSVVLSCSPSPMVRVTQTESSTPPGPG-SRQGPAMDGTAAEPRPGAGSLQH 60  
Qy 68 --AQQPPQPKRQRPEDFKFGKILGSGSFSTVLLARSLATSRYAIIKILSKRHIIKENKVP 125  
Db 61 HPAQLPQPKRQRPEDFKFGKILGSGSFSTVLLARSLATSRYAIIKILSKRHIIKENKVP 120  
Qy 126 YVTRERDVMRLDHPFFVKLYTTFQDDEKLYPGLSYAKGELLKYIRKIGSFDECTCFY 185  
Db 121 YVTRERDVMRLDHPFFVKLYTTFQDDEKLYPGLSYAKGELLKYIRKIGSFDECTCFY 180  
Qy 186 T A I V S A L E Y L G K G I I H R D L K P E N I L L N E D M H I Q I T D P G T A K V L S P E S K Q A R A N S F V G T 245  
Db 181 T A I V S A L E Y L G K G I I H R D L K P E N I L L N E D M H I Q I T D P G T A K V L S P E S K Q A R A N S F V G T 240  
Qy 246 A Q Y V S P E L L T E K S A C K S S D L M A L G C I I Y Q L V A G L P P F R A G N E Y L I P Q K I I K L E Y D F P E K F 305  
Db 241 A Q Y V S P E L L T E K S A C K S S D L M A L G C I I Y Q L V A G L P P F R A G N E Y L I P Q K I I K L E Y H P E K Y 300  
Qy 306 F P K A R D L V E K L L V D A T K R L G C E M E G Y P L K A H P F F T I T W N L H Q O T P P K I T A Y L P A M 365  
Db 301 F P K A R D L V E K L L V D A T K R L G C E M E G Y P L K A H P F F T I T W N L H Q O T P P K I T A Y L P A M 360  
Qy 366 S E D D E D C Y G N Y D N L S Q P G F M Q V S S S S S H S L S A S D T G L P O R S G S N I E Q Y I H D L D N S F E 425  
Db 361 S E D D E D C Y G N Y D N L S Q P G F M Q V S S S S S H S L S A S D T G L P O R S G S N I E Q Y I H D L D N S F E 420

Qy 426 LDLPSEDEKRLLEKQAGNPNPHQVNNLILKMGPDVKRGLFARRRQLLTGSPHLY 485  
Db 421 LDLPSEDEKRLLEKQAGNPNPHQVNNLILKMGPDVKRGLFARRRQLLTGSPHLY 480  
Qy 486 YVDPVNVKLGKIPMSQSLRPEAKNFKTFVHTPNRTTYLMDPSGNAHKCRKIQSVWRQ 545  
Db 481 YVDPVNVKLGKIPMSQSLRPEAKNFKTFVHTPNRTTYLMDPSGNAHKCRKIQSVWRQ 540  
Qy 546 RYQSHPDAAVQ 556  
Db 541 QYQSNPDAAVQ 551

#### RESULT 9

Q8K3L3\_MOUSE  
ID Q8K3L3\_MOUSE PRELIMINARY; PRT; 532 AA.  
AC Q8K3L3;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 21-FEB-2006, entry version 22.  
DE Phosphoinositide-dependent protein kinase-1 beta.  
GN Name=Pdk1; Synonyms=Pdk1beta;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22050196; PubMed=12054753; DOI=10.1016/S0006-291X(02)00449-7;  
RA Dong L.Q., Ramos F.J., Wick M.J., Lim M.A., Guo Z., Strong R.,  
RA Richardson A., Liu F.;  
RT "Cloning and characterization of a testis and brain-specific isoform  
of mouse 3'-phosphoinositide-dependent protein kinase-1, mPDK-1  
beta.";  
RL Biochem. Biophys. Res. Commun. 294:136-144(2002).  
CC -I- CATALYTIC ACTIVITY: ATP + a protein + ADP + a phosphoprotein.  
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL: AY062008; AAL47185.1; -. mRNA.  
DR HSSP: O15530; 1HIW.  
DR SMR: Q8K3L3; 48-134, 385-532.  
DR Ensembl: ENSMUSG00000024122; Mus musculus.  
DR MGI: MGI:1338068; Pdk1.  
DR GO: GO:0005737; Cytoplasm; IDA.  
DR GO: GO:0016023; Cytoplasmic membrane-bound vesicle; IDA.  
DR GO: GO:0004676; P:3-phosphoinositide-dependent protein kinase. . .; IDA.  
DR GO: GO:0006972; P:hyperosmotic response; IDA.  
DR GO: GO:0007165; P:signal transduction; TAS.  
DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.

DT 15-MAR-2005, sequence version 1.  
DT 21-FEB-2006, entry version 10.  
DE Hypothetical protein.  
GN ORFNames=RCJMB04\_6p10;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA STRAIN=CB; TISSUE=Bursa;  
RC Caldwell R.B., Kierzek A.M., Arakawa K., Bezzubov Y., Zaim J.,  
RA Fiedler P., Kutter S., Blagoderaki A., Kostovska D., Koter M.,  
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;  
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate  
gene function analysis.";  
RL Genome Biol. 6:R6-R6(2005).  
CC -I- CATALYTIC ACTIVITY: ATP + a protein + ADP + a phosphoprotein.  
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL: AJ851556; CAH65190.1; -. mRNA.  
DR SMR: Q5F3U4; 75-361, 412-555.  
DR GO: GO:0005524; P:ATP binding; IEA.  
DR GO: GO:0001666; P:nucleotide binding; IEA.  
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; P:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR011993; PH\_type.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Kinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 556 AA; 63068 MW; 81ED935D6C3E04C9 CRC64;

Query Match 89.3%; Score 2626.5; DB 2; Length 556;  
Best Local Similarity 90.5%; Pred. No. 1.5e-163;  
Matches 504; Conservative 15; Mismatches 33; Indels 5; Gaps 4;

Qy 1 MASTSSLYDAVPIQSSVVLCSPPSMVRNQAESTPVSISTQSSRQSNMESTAAESR 59  
Db 1 MASTSSLYDAVPIQSSVVLCSPPSMVRNQAESTPVSISTQSSRQSNMESTAAESR 60  
Qy 60 PGAGSL-QH-AQPPQPRKIKRDPDPKPKILGSGSFTVVLARELTSSREYAIKLEKRX 117  
Db 61 SSNSLPGHTQGPQPRKIKRDPDPKPKILGSGSFTVVLARELTSSREYAIKLEKRX 120

DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Kinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 532 AA; 60934 MW; F90731C7ECDE589 CRC64;

Query Match 89.3%; Score 2626.5; DB 2; Length 532;  
Best Local Similarity 94.2%; Pred. No. 1.4e-163;  
Matches 501; Conservative 9; Mismatches 19; Indels 3; Gaps 2;

Qy 28 MVRTQTESSTPPGIPGG-SRQSPAMDQTAASPRGAGSLQH--AQPPQPRKIKRDPDPK 84  
Db 1 MVRTQTESSTPPGIPGG-SRQSPAMDQTAASPRGAGSLQH--AQPPQPRKIKRDPDPK 60  
Qy 85 GKILGSGSFTVVLARELTSSREYAIKLEKRXI IKENKVPVYTRDRVMSRLDHPFVK 144  
Db 61 GKILGSGSFTVVLARELTSSREYAIKLEKRXI IKENKVPVYTRDRVMSRLDHPFVK 120  
Qy 145 LYFTFQDDKLYPGLSYAKNGELLKYIKIGSFDCTRPTTASIVSALEYLHGKQI IHR 204  
Db 121 LYFTFQDDKLYPGLSYAKNGELLKYIKIGSFDCTRPTTASIVSALEYLHGKQI IHR 180  
Qy 205 DLKPFENILNEDMHQIQTDFGTAKVLSPEKQARANSFVGTAGTVSPELLTEKSACKSSD 264  
Db 181 DLKPFENILNEDMHQIQTDFGTAKVLSPEKQARANSFVGTAGTVSPELLTEKSACKSSD 240  
Qy 265 LNALGCIYQLVAGLPFPFRAGNSYLIPOKIIKLEYHPPKFPFKARDLVEKLLVLDATKR 324  
Db 241 LNALGCIYQLVAGLPFPFRAGNSYLIPOKIIKLEYHPPKFPFKARDLVEKLLVLDATKR 300  
Qy 325 LGCSEMGYGLKAHPFFSVTWENLHQOTPPKLTATLPAKSEDDDCYGNLMDLSQFG 384  
Db 301 LGCSEMGYGLKAHPFFSVTWENLHQOTPPKLTATLPAKSEDDDCYGNLMDLSQFG 360  
Qy 385 CMQVSSSSSHLSASDTGLPQSSGSIHQYIHDLNNSFELDLPQSSDESKRLLEKQAG 444  
Db 361 CMQVSSSSSHLSVETSLPQSSGSIHQYIHDLNNSFELDLPQSSDESKRLLEKQAG 420  
Qy 445 GNPHQFVNNLILKMGPDVKRGLFARRRQLLTGSPHLYYVDPVNVKLGKIPMSQSL 504  
Db 421 GNPHQFVNNLILKMGPDVKRGLFARRRQLLTGSPHLYYVDPVNVKLGKIPMSQSL 480  
Qy 505 RPEAKNFKTFVHTPNRTTYLMDPSGNAHKCRKIQSVWRQYQSHPDAAVQ 556  
Db 481 RPEAKNFKTFVHTPNRTTYLMDPSGNAHKCRKIQSVWRQYQSHPDAAVQ 532

#### RESULT 10

Q5F3U4\_CHECK  
ID Q5F3U4\_CHECK PRELIMINARY; PRT; 556 AA.  
AC Q5F3U4;  
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.

Qy 118 I IKENKVPVYTRDRVMSRLDHPFVKLYFTFQDDKLYPGLSYAKNGELLKYIKIGSF 177  
Db 121 I IKENKVPVYTRDRVMSRLDHPFVKLYFTFQDDKLYPGLSYAKNGELLKYIKIGSF 180  
Qy 178 DDTCTRPTTASIVSALEYLHGKQI IHRDLKPFENILNEDMHQIQTDFGTAKVLSPEKQA 237  
Db 181 DDTCTRPTTASIVSALEYLHGKQI IHRDLKPFENILNEDMHQIQTDFGTAKVLSPEKQA 240  
Qy 238 RANSFVGTAGTVSPELLTEKSACKSSDLNALGCIYQLVAGLPFPFRAGNSYLIPOKIIK 297  
Db 241 RANSFVGTAGTVSPELLTEKSACKSSDLNALGCIYQLVAGLPFPFRAGNSYLIPOKIIK 300  
Qy 298 EYDFPFKFPFKARDLVEKLLVLDATKRLGCEMGYGLKAHPFFSVTWENLHQOTPPK 357  
Db 301 EYDFPFKFPFKARDLVEKLLVLDATKRLGCEMGYGLKAHPFFSVTWENLHQOTPPK 360  
Qy 358 LTATLPAKSEDDDCYGNLMDLSQFGCMQVSSSSSHLSASDTGLPQSSGSIHQYIH 417  
Db 361 LTATLPAKSEDDDCYGNLMDLSQFGCMQVSSSSSHLSVETSLPQSSGSIHQYIH 420  
Qy 418 DLDNSFELDLPQSSDESKRLLEKQAGGNPHQFVNNLILKMGPDVKRGLFARRRQL 477  
Db 421 DLDNSFELDLPQSSDESKRLLEKQAGGNPHQFVNNLILKMGPDVKRGLFARRRQL 480  
Qy 478 LTGSPHLYYVDPVNVKLGKIPMSQSLRPEAKNFKTFVHTPNRTTYLMDPSGNAHKCR 537  
Db 481 LTGSPHLYYVDPVNVKLGKIPMSQSLRPEAKNFKTFVHTPNRTTYLMDPSGNAHKCR 540  
Qy 538 KIQSVWRQYQSHPDAA 554  
Db 541 KIQSVWRURY--HQWAA 555

#### RESULT 11

Q3TRL2\_MOUSE  
ID Q3TRL2\_MOUSE PRELIMINARY; PRT; 522 AA.  
AC Q3TRL2;  
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
DT 11-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Adult female vagina cDNA, RIKEN full-length enriched library.  
DE clone:9930010N10 product:3-phosphoinositide dependent protein kinase-  
DE 1, full insert sequence.  
GN Name=Pdpk1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Vagina;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).



RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Desilva C., Salameh M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Rubin C., Castelli V., Katinka M., Vacherie S.,  
RA Biemont C., Skalli Z., Cattolico L., Poulsen J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brothier P., Coutanceau J.-P., Gouzy J.,  
RA Parra G., Lardier G., Chappia C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.-M., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin M., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,  
RT \*Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.\*  
RL Nature 431:946-957(2004).  
RM (2)  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Center for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell  
CC cycle. It is required in higher cells for entry into S-phase and  
CC mitosis. Component of the kinase complex that phosphorylates the  
CC respective C-terminus of RNA polymerase II. Catalytic component of  
CC MPF (by similarity).  
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
CC mature oocytes (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; CAAG01014738; CAG04372.1; -, Genomic DNA.  
DR SMR; QMS480; 78-364, 417-557.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:0000166; P:nucleotide binding; IEA.  
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Kinase; 1.  
DR ProDom; PD0000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
FT NON\_TER 558 558  
SQ SEQUENCE 558 AA; 63806 MW; 4E0997DA7344C73A CRC64;  
  
Query Match 81.3%; Score 2391.5; DB 2; Length 558;  
Best Local Similarity 81.7%; Pred. No. 3.7e-148;  
Matches 455; Conservative 43; Mismatches 52; Indels 7; Gaps 4;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPSVRTTOTESSTPPGIPGSGR-QGPAMDGTAAAPR 59  
Db 1 MARATSQLYDVVPIQSSVVLSCSPSPSVRTTOTESSTPPGIPGSGR-QGPAMDGTAAAPR 60  
  
Oy 60 ----PGAGSLQHAQPP-PPRKRKPEDPKFGKILGSGSPSTVVLARELATSREYAIKILK 114  
Db 61 LDGASGSGTQAAAPPPQPKKQKQSPDFKFGKILGSGSPSTVVLARELATSREYAIKILK 120  
  
Oy 115 KRHIKENKVPYVTRERDMSRLDHPFVKLYPTQDDKLYPGLSYAKGSLKLYIRKI 174  
Db 121 KRHIKENKVPYVTRERDMSRLDHPFVKLYPTQDDKLYPGLSYAKGSLKLYIRKI 180  
  
Oy 175 GSPFTCTRPYTAIVSALSYLHGKIIHRDLKPEINLLNEDMHIQITDPTAKVLSPE 234  
Db 181 GSPFTCTRPYTAIVSALSYLHGKIIHRDLKPEINLLNEDMHIQITDPTAKVLSPE 240  
  
Oy 235 KOARANSFVGTAYVSPPELLTEKSACKSDMLALGCIYQLVAGLPPFRAGNEYLIPOKI 294  
Db 241 KOARANSFVGTAYVSPPELLTEKSACKSDMLALGCIYQLVAGLPPFRAGNEYLIPOKI 300  
  
Oy 295 IKLEYDFPEKFPFKARDLVEKLLVLDATKRLGCEMGGYGLKHAHPFESVTWNLHQOT 354  
Db 301 IKLEYDFPEKFPFKARDLVEKLLVLDATKRLGCEMGGYGLKHAHPFESVTWNLHQOT 360  
  
Oy 355 PPKLTAYLPAKSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQRSQSWIB 413  
Db 361 PPKLTAYLPAKSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQRSQSWIB 420  
  
Oy 414 QYIHDLNNSFELDLQFSEDEKRLLEKQAGNTPHGVFNENILJMGVDPDKRGLFARR 473  
Db 421 QYIHDLNNSFELDLQFSEDEKRLLEKQAGNTPHGVFNENILJMGVDPDKRGLFARR 480  
  
Oy 474 ROLLTSPHLYVVDVNVKLGKSIWMSQLRPEAKNFKTFFVHTPNRTTYLMDPSGNH 533  
Db 481 ROLLTSPHLYVVDVNVKLGKSIWMSQLRPEAKNFKTFFVHTPNRTTYLMDPSGNH 540  
  
Oy 534 KRCIKIQVWRQYQSH 550  
Db 541 KRCIKIQVWRQYQSH 557

RESULT 13  
Q59EH6 HUMAN  
ID Q59EH6 HUMAN PRELIMINARY; PRT; 492 AA.  
AC Q59EH6;  
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
DT 26-APR-2005, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE 3-phosphoinositide dependent protein kinase-1 variant (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Brain;  
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,  
RA Ohara O., Nagase T., Kikuno F.R.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AB209835; BAD93072.1; -, mRNA.  
DR SMR; Q59EH6; 110-396.  
DR Ensembl; ENSG00000104992; Homo sapiens.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:0000166; P:nucleotide binding; IEA.  
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000169; Pept\_cys\_AS.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00139; THIOLESTERASE\_CYS; UNKNOWN\_1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
FT NON\_TER 1 1  
SQ SEQUENCE 492 AA; 54828 MW; A8BA2A6F7C98E26 CRC64;  
  
Query Match 79.4%; Score 2336; DB 2; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.4e-144;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPSVRTTOTESSTPPGIPGSGRQGPAMDGTAAAPR 60  
Db 39 MARTTSQLYDAVPIQSSVVLSCSPSPSVRTTOTESSTPPGIPGSGRQGPAMDGTAAAPR 98  
  
Oy 61 GAGSLQHAQPPPPRKRKPEDPKFGKILGSGSPSTVVLARELATSREYAIKILKRIK 120  
Db 99 GAGSLQHAQPPPPRKRKPEDPKFGKILGSGSPSTVVLARELATSREYAIKILKRIK 158  
  
Oy 121 ENKVPYVTRERDMSRLDHPFVKLYPTQDDKLYPGLSYAKGSLKLYIRKISGPD 180  
Db 159 ENKVPYVTRERDMSRLDHPFVKLYPTQDDKLYPGLSYAKGSLKLYIRKISGPD 218  
  
Oy 181 CTRPYTAIVSALSYLHGKIIHRDLKPEINLLNEDMHIQITDPTAKVLSPEKQARAN 248  
Db 219 CTRPYTAIVSALSYLHGKIIHRDLKPEINLLNEDMHIQITDPTAKVLSPEKQARAN 278  
  
Oy 241 SPVGTAYVSPPELLTEKSACKSDMLALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Db 279 SPVGTAYVSPPELLTEKSACKSDMLALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 338

Oy 301 PPEKFPFKARDLVEKLLVLDATKRLGCEMGGYGLKHAHPFESVTWNLHQOTPPKILTA 360  
Db 339 PPEKFPFKARDLVEKLLVLDATKRLGCEMGGYGLKHAHPFESVTWNLHQOTPPKILTA 398  
  
Oy 361 YLPAMSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQRSQSWIBQYIHDL 420  
Db 399 YLPAMSEDDDCYGYDNLISQPGCHQVSSSSSSSLASD-TGLPQRSQSWIBQYIHDL 458  
  
Oy 421 SNSFELDLQFSEDEKRLLEKQAGN 447  
Db 459 SNSFELDLQFSEDEKRLLEKQAGN 485

RESULT 14  
Q6NZV1 BRARE  
ID Q6NZV1 BRARE PRELIMINARY; PRT; 537 AA.  
AC Q6NZV1;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 21-FEB-2006, entry version 20.  
DE Hypothetical protein zgc:77318.  
GN ORFNames-zgc:77318;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
RA Dischenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Umed T.B., Tomihata K., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren S.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kattaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blekesley R.M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smaluk D.S.,  
RA Schneringer A., Schein J.E., Jones S.J.M., Marz M.A.;  
RT \*Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.\*  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RG NIH MGC Project;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

Qy	1	MARTTSQLDVAVPIGQSSVVLCS	CPSPMVR	TQESSTP	PGIGS	RQGP	AKDQ	TAAE	PPR	60	
Db	1	MARTTSQLDVAVPIGQSSVVLCS	CPSPMVR	TQESSTP	PGIGS	RQGP	AKDQ	TAAE	PPR	60	
Qy	61	GAQS	LQHAQPP	PPQPKR	PE	DF	KG	IL	GG	STV	120
Db	61	GAQS	LQHAQPP	PPQPKR	PE	DF	KG	IL	GG	STV	109
Qy	121	ENKVP	YPTV	TRER	DM	SR	LH	DP	VP	VK	180
Db	110	-----	-----	-----	-----	-----	-----	-----	-----	-----	109
Qy	181	CTR	PYTAS	IV	SAL	SYL	H	KG	GI	I	240
Db	110	-----	-----	-----	-----	-----	-----	-----	-----	-----	240
Qy	241	SPVGT	AAQY	SP	ELL	TK	SK	SS	DL	NAL	300
Db	241	SPVGT	AAQY	SP	ELL	TK	SK	SS	DL	NAL	300
Qy	241	SPVGT	AAQY	SP	ELL	TK	SK	SS	DL	NAL	300
Db	241	SPVGT	AAQY	SP	ELL	TK	SK	SS	DL	NAL	300

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RESULT 15
Q9BRD5_HUMAN
ID Q9BRD5_HUMAN PRELIMINARY; PRT; 429 AA.
AC Q9BRD5; Q8I5V2;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2004, sequence version 2.
DT 07-FEB-2006, entry version 29.
DE 3-phosphoinositide dependent protein kinase-1 (PDPK1 protein).
GN Name=PDPK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain, and Uterus;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavent T.L., Scheetz T.S.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locoanello N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Gordergen E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R., Madison E., Young A.C., Shvetchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalka U., Smolus D.S.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT *Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.*
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

```

Qy	301	FPEKFPKARDLVKLLVLVDATIKRLGCEBMGYGPKLKAHPFPFESVTWNLHMQTPPKLTA	360
Db	174	FPEKFPKARDLVKLLVLVDATIKRLGCEBMGYGPKLKAHPFPFESVTWNLHMQTPPKLTA	233
Qy	361	YLPAMSEDEDDCYGNYDNLISQPGCMQVSSSSSHLSASDGTGLPQRSGSNIQYIHDL	420
Db	234	YLPAMSEDEDDCYGNYDNLISQPGCMQVSSSSSHLSASDGTGLPQRSGSNIQYIHDL	293
Qy	421	SNSFELDLQFSDEKRLLLSKQAGGNPWHQPVENNLILOGPVDKRGKGLFARRRQLLTS	480
Db	294	SNSFELDLQFSDEKRLLLSKQAGGNPWHQPVENNLILOGPVDKRGKGLFARRRQLLTS	353
Qy	481	GHLYYVDPNKVLKGSIPMSGLAPLAEAGNFKTFPVHTPRITYLADPSONAHKWRCKIQ	540
Db	354	GHLYYVDPNKVLKGSIPMSGLAPLAEAGNFKTFPVHTPRITYLADPSONAHKWRCKIQ	413
Qy	541	SVWRORYGSHPDAAVQ	556
Db	414	SVWRORYGSHPDAAVQ	429

Search completed: June 27, 2006, 01:36:19  
Job time : 302 sec

OM protein - protein search, using sw model

Run on: June 26, 2006, 23:38:12 ; Search time 196 Seconds  
(without alignments)  
1297.002 Million cell updates/sec

Title: US-10-689-576-1  
Perfect score: 2941  
Sequence: 1 MARTTSQLYDAVPIQSSVVL.....RKIQSVWRQRYQSHPDAAVQ 556

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseq1980a:\*  
2: geneseq1990a:\*  
3: geneseq2000a:\*  
4: geneseq2001a:\*  
5: geneseq2002a:\*  
6: geneseq2003a:\*  
7: geneseq2003ba:\*  
8: geneseq2004a:\*  
9: geneseq2005a:\*  
10: geneseq2006a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2941	100.0	556	2 AAW71738	Aaw71738 Human 3-p
2	2941	100.0	556	2 AAY27055	Aay27055 Human pro
3	2941	100.0	556	3 AAB28445	Aab28445 Human PDK
4	2941	100.0	556	3 AAB28446	Aab28446 Human PDK
5	2941	100.0	556	3 AAY94735	Aay94735 Phosphoin
6	2941	100.0	556	6 ABO07176	Abu07176 Human p53
7	2941	100.0	556	6 ABU04708	Abu04708 Human exp

XX  
PN WO9841638-A1.  
XX  
PD 24-SEP-1998.  
XX  
PF 16-MAR-1998; 98WO-GB000777.  
XX  
PR 17-MAR-1997; 97GB-00005462.  
PR 19-JUN-1997; 97GB-00012826.  
PR 15-AUG-1997; 97GB-00017253.  
PR 03-OCT-1997; 97US-00943667.  
XX  
PA (MEDI-) MEDICAL RES COUNCIL.  
XX  
PI Alessi DR;  
XX  
DR WPI; 1998-531572/45.  
DR N-PSDB; AAV61037.  
XX  
PT New isolated 3-phosphoinositide-dependent protein kinase - which  
PT phosphorylates and activates protein kinase B-alpha, used to develop  
PT products for treating diabetes or cancers or for enhancing cell  
PT proliferation.  
XX  
PS Example 2; Fig 10; 120pp; English.  
XX  
CC A pure 3-phosphoinositide-dependent protein kinase (3PDPK) that  
CC phosphorylates and activates PK B-alpha has been isolated. The present  
CC sequence represents human 3PDPK. Products from the present invention  
CC (e.g. 3PDPK, nucleotide sequence encoding 3PDPK, antibodies against  
CC 3PDPK) can be used to identify compounds which modulate the PK activity  
CC e.g. for treating diabetes or cancers or for enhancing cell proliferation  
CC in the regeneration of nerves or in wound healing  
XX  
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCPSPSMVRTTSTPGIPGGSROGPAMDQAAEPRP 60  
|||||  
Db 1 MARTTSQLYDAVPIQSSVVLSCPSPSMVRTTSTPGIPGGSROGPAMDQAAEPRP 60  
Oy 61 GAGSLQHAQPPQPRQPRPDKPGKILGEGSFSTVVLARELATSREYAIKILKRIHIK 120  
|||||  
Db 61 GAGSLQHAQPPQPRQPRPDKPGKILGEGSFSTVVLARELATSREYAIKILKRIHIK 120  
Oy 121 ENKVPVYTRERDMSRLDHPFFVKLYPTQDDKLYFGLSYAKGELLKYIRKIGSFDET 180  
|||||  
Db 121 ENKVPVYTRERDMSRLDHPFFVKLYPTQDDKLYFGLSYAKGELLKYIRKIGSFDET 180  
Oy 181 CTRPYTARIVSALEYLHGKIIRDLKPEINLLNEDMKIQTDPGTAKVLSPESKQARAN 240  
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Db 181 CTRPYTARIVSALEYLHGKIIRDLKPEINLLNEDMKIQTDPGTAKVLSPESKQARAN 240  
Oy 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNYLI FOKI I KLEBYD 300

8	2941	100.0	556	6 ABU04718	Abu04718 Human exp
9	2941	100.0	556	6 ABU04712	Abu04712 Human exp
10	2941	100.0	556	6 ABU04716	Abu04716 Human exp
11	2941	100.0	556	6 ABU04711	Abu04711 Human exp
12	2941	100.0	556	6 ABU04706	Abu04706 Human exp
13	2941	100.0	556	6 ABU04714	Abu04714 Human exp
14	2941	100.0	556	6 ABU04707	Abu04707 Human exp
15	2941	100.0	556	6 ABU04717	Abu04717 Human exp
16	2941	100.0	556	7 ABM79012	Abm79012 Human pho
17	2941	100.0	556	7 ADD44919	Add44919 Human Pro
18	2941	100.0	556	7 ADD44915	Add44915 Human Pro
19	2941	100.0	556	7 ADD89983	Add89983 Human can
20	2941	100.0	556	8 ADI36055	Adi36055 Human pho
21	2941	100.0	556	8 ADI36055	Adi36055 Human pho
22	2941	100.0	556	8 ADQ19234	Adq19234 Human eof
23	2937	99.9	556	2 AAY05779	Aay05779 Human pro
24	2889.5	98.2	599	8 ABM84519	Abm84519 Human dia
25	2838	96.5	535	4 AAB99823	Aab99823 AGC prote
26	2838	96.5	535	6 ABU04713	Abu04713 Human exp
27	2787.5	94.8	559	7 ADD44917	Add44917 Rat Prote
28	2787.5	94.8	559	7 ADD44913	Add44913 Rat Prote
29	2682	91.2	506	2 AAY05780	Aay05780 Human pro
30	2682	91.2	506	6 ABU04715	Abu04715 Human exp
31	2360	80.2	462	10 AEF60044	Aef60044 Human tru
32	2202.5	74.9	468	6 ABU04719	Abu04719 Human exp
33	2202.5	74.9	468	6 ABU04705	Abu04705 Human exp
34	1893	64.4	361	9 ADY85535	Ady85535 Catalytic
35	1747	59.4	335	4 AAB99847	Aab99847 AGC prote
36	1747	59.4	335	8 ADJ38895	Adj38895 PDK1 amin
37	1710	58.1	319	6 ABU04709	Abu04709 Human exp
38	1710	58.1	319	6 ABU04720	Abu04720 Human exp
39	1513	51.4	289	8 ADJ38865	Adj38865 PDK1 amin
40	1486	50.5	285	6 ABR57461	Abr57461 AGC fam1
41	1144.5	38.9	752	4 ABB57927	Abb57927 Drosophil
42	1144.5	38.9	752	4 ABB67127	Abb67127 Drosophil
43	1144.5	38.9	752	4 ABB57782	Abb57782 Drosophil
44	1144.5	38.9	752	4 ABB67126	Abb67126 Drosophil
45	973	33.1	539	4 ABB67129	Abb67129 Drosophil

ALIGNMENTS

RESULT 1

AAW71738  
ID AAW71738 standard; protein; 556 AA.  
XX  
AC AAW71738;  
XX  
DT 10-DEC-1998 (first entry)  
XX  
DE Human 3-phosphoinositide-dependent protein kinase.  
XX  
KW Protein kinase B-alpha; 3-phosphoinositide-dependent protein kinase;  
KW diabetes; cancer; cell proliferation; phosphorylation.  
XX  
OS Homo sapiens.

Db 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNYLI FOKI I KLEBYD 300  
Oy 301 FFSKFFPKARDLVEKLLVLVDATKRLGCESEMGYGLKAHPFFSVTWENLHQOTPPKLT 360  
Db 301 FFSKFFPKARDLVEKLLVLVDATKRLGCESEMGYGLKAHPFFSVTWENLHQOTPPKLT 360  
Oy 361 YLPAMSEDDDCYGNVDNLISQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420  
Db 361 YLPAMSEDDDCYGNVDNLISQFGCMQVSSSSSSSLASDTGLPQRSGSNIQYIHDLD 420  
Oy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQFVENNLI LKMGVPDKRGLPARRRQLLITE 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQFVENNLI LKMGVPDKRGLPARRRQLLITE 480  
Oy 481 GHILYYVDPVNKKVLKGSIPWSQSLRLEPAKNTKTFPVHTPNRTTYLMDPSNAHGWCKRIQ 540  
Db 481 GHILYYVDPVNKKVLKGSIPWSQSLRLEPAKNTKTFPVHTPNRTTYLMDPSNAHGWCKRIQ 540  
Oy 541 EVWRORYQSHPDAAVQ 556  
Db 541 EVWRORYQSHPDAAVQ 556

RESULT 2

AA27055  
ID AAY27055 standard; protein; 556 AA.  
XX  
AC AAY27055;  
XX  
DT 08-OCT-1999 (first entry)  
XX  
DE Human protein kinase (HPKM)-4 (clone ID 472480).  
XX  
KW Human protein kinase molecule; HPKM; human; protein kinase;  
KW phosphate group; cancer; immune disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO9931981-A2.  
XX  
PD 05-AUG-1999.  
XX  
PF 12-JAN-1999; 99WO-US000661.  
XX  
PR 30-JAN-1998; 98US-00016000.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
PI Bandman O, Hillman JL, Lal P, Akerblom IS, Shah P, Corley NC;  
PI Ouegler KJ;  
XX  
DR WPI; 1999-479190/40.  
DR N-PSDB; AAX89853.  
XX  
PT New human protein kinase molecules useful for treating or preventing  
PT cancer or an immune disorder.



XX  
PS Claim 1; Page 68-69; 77pp; English.  
XX  
CC The invention provides human protein kinase molecules (HPKM) (AAY27052-  
CC 57) and nucleic acid sequences (AAK89850-55) encoding the HPKM  
CC polypeptides respectively. The HPKM polypeptides can be produced  
CC recombinantly by standard recombinant methodology. Protein kinases add  
CC phosphate groups to proteins. HPKM polypeptide or an HPKM antagonist is  
CC used to treat or prevent cancer or an immune disorder. The present  
CC sequence represents the amino acid sequence of HPKM-4  
XX  
SQ Sequence 556 AA;  
  
Query Match 100.0%; Score 2941; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60  
  
Qy 61 GAGSLQHAQPPPPQPRKQRPEDPKFKGILGEGSFSTVVLARELATSREYAIIKLSKHIIK 120  
Db 61 GAGSLQHAQPPPPQPRKQRPEDPKFKGILGEGSFSTVVLARELATSREYAIIKLSKHIIK 120  
  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVQIYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVQIYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180  
  
Qy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240  
  
Qy 241 SFVQTAQVSPPELLTEKSACKSSDLWALGCIYYQLVAGLPPFRAGNEYLIFOKIILKLYD 300  
Db 241 SFVQTAQVSPPELLTEKSACKSSDLWALGCIYYQLVAGLPPFRAGNEYLIFOKIILKLYD 300  
  
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGLKQHPFFESVTWENLHQOTPPKLT 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMEGYGLKQHPFFESVTWENLHQOTPPKLT 360  
  
Qy 361 YLPAMSEDDDEDCYGNYNLLSQFGCMQVSSSSSHLSASDTGLPQSGSNIIEQYIHLD 420  
Db 361 YLPAMSEDDDEDCYGNYNLLSQFGCMQVSSSSSHLSASDTGLPQSGSNIIEQYIHLD 420  
  
Qy 421 SNSFELDLPSEDEKRLLLSKQAGGNPHQVNNLLIKMGVVDKRGKLFARRRQLLLT 480  
Db 421 SNSFELDLPSEDEKRLLLSKQAGGNPHQVNNLLIKMGVVDKRGKLFARRRQLLLT 480  
  
Qy 481 GPHLYYVDPVNKLKGBIPWSQLRPAKQNFKTFPVHTPNRTYYLMDPSGNAHWCKRIQ 540  
Db 481 GPHLYYVDPVNKLKGBIPWSQLRPAKQNFKTFPVHTPNRTYYLMDPSGNAHWCKRIQ 540  
  
Qy 541 EVWRQRYQSHPDAAVQ 556  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 4  
AAB28446  
ID AAB28446 standard; protein; 556 AA.  
XX  
AC AAB28446;  
XX  
DT 01-FEB-2001 (first entry)  
XX  
DE Human PDK-1.  
XX  
KW Human; PDK-1; 3-phosphoinositide dependent protein kinase-1;  
KW antisense oligonucleotide; phosphorothioate; antiinflammatory;  
KW cytostatic; antimicrobial.  
XX  
OS Homo sapiens.  
XX  
PN US6124272-A.

RESULT 3  
AAB28445  
ID AAB28445 standard; protein; 556 AA.  
XX  
AC AAB28445;  
XX  
DT 01-FEB-2001 (first entry)  
XX  
DE Human PDK-1.  
XX  
KW Human; PDK-1; 3-phosphoinositide dependent protein kinase-1;  
KW antisense oligonucleotide; phosphorothioate; antiinflammatory;  
KW cytostatic; antimicrobial.  
XX  
OS Homo sapiens.  
XX  
PN US6124272-A.  
XX  
PD 26-SEP-2000.  
XX  
PF 09-APR-1999; 99US-00289466.  
XX  
PR 09-APR-1999; 99US-00289466.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monie BP, Cowseert LM;  
XX  
DR WPI; 2000-611015/58.  
DR N-PSDB; AAC60590.  
XX  
PT Novel antisense compounds useful for inhibiting the expression of human 3  
PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating  
PT inflammation, tumors and infections.  
XX  
PS Disclosure; Col 45-48; 41pp; English.  
XX  
CC The nucleotide sequence encoding the present protein was used to design a  
CC large number of antisense oligonucleotides which are targeted to a  
CC nucleic acid molecule encoding human 3-phosphoinositide dependent protein  
CC kinase-1 (PDK-1). The antisense compounds may be oligodeoxynucleotides or  
CC chimeric oligonucleotides containing a central gap region, consisting of  
CC ten 2'-deoxynucleotides, which is flanked on both sides by 2'-  
CC methoxyethyl (2'-MOE) wings. The oligonucleotides have a phosphorothioate  
CC backbone. The antisense oligonucleotides are useful for inhibiting the  
CC expression of human PDK-1 in human cells or tissues. They are also useful  
CC for preventing or delaying infection, inflammation or tumors and are  
CC useful for research and diagnostics  
XX  
SQ Sequence 556 AA;  
  
Query Match 100.0%; Score 2941; DB 3; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60

XX  
PD 26-SEP-2000.  
XX  
PF 09-APR-1999; 99US-00289466.  
XX  
PR 09-APR-1999; 99US-00289466.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monie BP, Cowseert LM;  
XX  
DR WPI; 2000-611015/58.  
DR N-PSDB; AAC60591.  
XX  
PT Novel antisense compounds useful for inhibiting the expression of human 3  
PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating  
PT inflammation, tumors and infections.  
XX  
PS Disclosure; Col 49-52; 41pp; English.  
XX  
CC The nucleotide sequence encoding the present protein was used to design a  
CC large number of antisense oligonucleotides which are targeted to a  
CC nucleic acid molecule encoding human 3-phosphoinositide dependent protein  
CC kinase-1 (PDK-1). The antisense compounds may be oligodeoxynucleotides or  
CC chimeric oligonucleotides containing a central gap region, consisting of  
CC ten 2'-deoxynucleotides, which is flanked on both sides by 2'-  
CC methoxyethyl (2'-MOE) wings. The oligonucleotides have a phosphorothioate  
CC backbone. The antisense oligonucleotides are useful for inhibiting the  
CC expression of human PDK-1 in human cells or tissues. They are also useful  
CC for preventing or delaying infection, inflammation or tumors and are  
CC useful for research and diagnostics  
XX  
SQ Sequence 556 AA;  
  
Query Match 100.0%; Score 2941; DB 3; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60  
  
Qy 61 GAGSLQHAQPPPPQPRKQRPEDPKFKGILGEGSFSTVVLARELATSREYAIIKLSKHIIK 120  
Db 61 GAGSLQHAQPPPPQPRKQRPEDPKFKGILGEGSFSTVVLARELATSREYAIIKLSKHIIK 120  
  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVQIYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVQIYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180  
  
Qy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240  
  
Qy 241 SFVQTAQVSPPELLTEKSACKSSDLWALGCIYYQLVAGLPPFRAGNEYLIFOKIILKLYD 300  
Db 241 SFVQTAQVSPPELLTEKSACKSSDLWALGCIYYQLVAGLPPFRAGNEYLIFOKIILKLYD 300

XX  
PD 26-SEP-2000.  
XX  
PF 09-APR-1999; 99US-00289466.  
XX  
PR 09-APR-1999; 99US-00289466.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monie BP, Cowseert LM;  
XX  
DR WPI; 2000-611015/58.  
DR N-PSDB; AAC60591.  
XX  
PT Novel antisense compounds useful for inhibiting the expression of human 3  
PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating  
PT inflammation, tumors and infections.  
XX  
PS Disclosure; Col 49-52; 41pp; English.  
XX  
CC The nucleotide sequence encoding the present protein was used to design a  
CC large number of antisense oligonucleotides which are targeted to a  
CC nucleic acid molecule encoding human 3-phosphoinositide dependent protein  
CC kinase-1 (PDK-1). The antisense compounds may be oligodeoxynucleotides or  
CC chimeric oligonucleotides containing a central gap region, consisting of  
CC ten 2'-deoxynucleotides, which is flanked on both sides by 2'-  
CC methoxyethyl (2'-MOE) wings. The oligonucleotides have a phosphorothioate  
CC backbone. The antisense oligonucleotides are useful for inhibiting the  
CC expression of human PDK-1 in human cells or tissues. They are also useful  
CC for preventing or delaying infection, inflammation or tumors and are  
CC useful for research and diagnostics  
XX  
SQ Sequence 556 AA;  
  
Query Match 100.0%; Score 2941; DB 3; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSMVRTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60  
  
Qy 61 GAGSLQHAQPPPPQPRKQRPEDPKFKGILGEGSFSTVVLARELATSREYAIIKLSKHIIK 120  
Db 61 GAGSLQHAQPPPPQPRKQRPEDPKFKGILGEGSFSTVVLARELATSREYAIIKLSKHIIK 120  
  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVQIYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVQIYPTQDDSKLYPGLSYAKNGELLKYIRKIGSFDET 180  
  
Qy 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240  
Db 181 CTRFYTAIVSALEYLHGKGIHRDLKPENILLNEDMHQIOTDPTAKVLSPEKQARAN 240  
  
Qy 241 SFVQTAQVSPPELLTEKSACKSSDLWALGCIYYQLVAGLPPFRAGNEYLIFOKIILKLYD 300  
Db 241 SFVQTAQVSPPELLTEKSACKSSDLWALGCIYYQLVAGLPPFRAGNEYLIFOKIILKLYD 300

Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSNIEQYIHDL 420  
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSNIEQYIHDL 420  
Qy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQFVENNLILQMGVDPDKRGLPARRRQLL 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQFVENNLILQMGVDPDKRGLPARRRQLL 480  
Qy 481 GPHLYYVDPVNVKLGSIWMSQLRPAQNFKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Db 481 GPHLYYVDPVNVKLGSIWMSQLRPAQNFKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Qy 541 EVMRORYQSHPDAAVO 556  
Db 541 EVMRORYQSHPDAAVO 556

RESULT 5

AAI94735  
ID AAI94735 standard; protein; 556 AA.  
XX  
AC AAI94735;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Phosphoinositide dependent protein kinase 1 (PDK1).  
XX  
KW Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1;  
KW protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;  
KW mechanical tissue damage; ischaemic disease; stroke;  
KW myocardial infarction; antigenic peptide.  
XX  
OS Unidentified.  
XX  
PN W0200056864-A2.  
XX  
PD 28-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-GB001004.  
XX  
PR 19-MAR-1999; 99GB-00006245.  
XX  
PA (UYDU-) UNIV DUNDSE.  
XX  
PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;  
XX  
DR WPI; 2000-647155/62.  
XX  
PT Altering substrate specificity of phosphoinositide-dependent protein  
PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to  
PT interacting polypeptide.  
XX

Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGPLKQHPFESVTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSNIEQYIHDL 420  
Db 361 YLPAMSEDDSDCYGNYNLLSQPGCMQVSSSSSSSLASDTGLPQRSNIEQYIHDL 420  
Qy 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQFVENNLILQMGVDPDKRGLPARRRQLL 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPMHQFVENNLILQMGVDPDKRGLPARRRQLL 480  
Qy 481 GPHLYYVDPVNVKLGSIWMSQLRPAQNFKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Db 481 GPHLYYVDPVNVKLGSIWMSQLRPAQNFKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Qy 541 EVMRORYQSHPDAAVO 556  
Db 541 EVMRORYQSHPDAAVO 556

RESULT 6

AB007176  
ID AB007176 standard; protein; 556 AA.  
XX  
AC AB007176;  
XX  
DT 13-AUG-2003 (first entry)  
XX  
DE Human p53 modifying protein, SEQ ID 136.  
XX  
KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;  
KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;  
KW lung cancer; ovarian cancer; angiogenesis; cell cycle;  
KW apoptotic disorder; cell proliferation disorder.  
XX  
OS Homo sapiens.  
XX  
PN W0200299122-A1.  
XX  
PD 12-DEC-2002.  
XX  
PF 03-JUN-2002; 2002WO-US017382.  
XX  
PR 05-JUN-2001; 2001US-0296076P.  
PR 10-OCT-2001; 2001US-0328605P.  
PR 15-FEB-2002; 2002US-0357253P.  
XX  
PA (EXSL-) EXSLIXIS INC.  
XX  
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Panka RP;  
XX  
DR WPI; 2003-156859/15.  
DR N-PDB; ACD13352.  
XX  
PT Identifying modulators of the p53 pathway for use in treating apoptotic  
PT or cell proliferation disorders, comprises screening for agents that

PS Disclosure; Fig 10; 103pp; English.

XX  
CC This invention relates to a method for altering the substrate specificity  
CC of phosphoinositide-dependent protein kinase 1 (PDK1), by exposing it to  
CC an interacting polypeptide. Included in the invention are a preparation  
CC comprising PDK1 and an interacting polypeptide, PDK1 with altered  
CC specificity is useful for phosphorylating a residue corresponding to the  
CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa  
CC -Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for phosphorylating  
CC protein kinase C related protein kinase 2 (PRK2). The compound identified  
CC by methods of the invention that are capable of altering the substrate  
CC specificity of PDK1 are useful for manufacturing a medicament for  
CC treating a patient who is in need of modulation of the insulin signalling  
CC pathway and/or PDK1, PDK2 or PRK2 signalling. A compound that is capable  
CC of reducing the activity (i.e. the PDK1 and/or the PDK2 activity) of PDK1  
CC may be useful in treating cancer. PDK1, e.g. via protein kinase B and/or  
CC SGK, may be capable of providing a survival signal that protects cells  
CC from apoptosis induced in a variety of ways. Reduction of the activity of  
CC PDK1 may promote apoptosis and may be useful in treating cancer.  
CC Conditions in which aiding apoptosis may be benefit may also include  
CC resolution of inflammation. A compound capable of increasing the activity  
CC of PDK1 may be useful in treating diabetes or obesity, or may be useful  
CC in inhibiting apoptosis. Increased activity of PDK1 may lead to increased  
CC levels of leptin, which may lead to weight loss. The compounds may  
CC suppress apoptosis, which may aid cell survival during or following cell  
CC damaging processes and in treating disease in which apoptosis is  
CC involved. Examples of the diseases include, mechanical (including heat)  
CC tissue injury or ischaemic disease, for example stroke and myocardial  
CC infarction, or neural injury. The present sequence represents a  
XX phosphoinositide-dependent-protein kinase 1 amino acid sequence  
XX  
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 3; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSCPSPMVRVTSSTPPGPGGSRQGPAMQGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSCPSPMVRVTSSTPPGPGGSRQGPAMQGTAAEPRP 60  
Qy 61 GAGSLQHAQPPPPQPKRKPEDPKFKGKILGEGSPSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQHAQPPPPQPKRKPEDPKFKGKILGEGSPSTVVLARELATSREYAIKILEKRII 120  
Qy 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYPLGSLYAKNGSLKYIKIGSFDET 180  
Db 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYPLGSLYAKNGSLKYIKIGSFDET 180  
Qy 181 CTRFYTABIVSALEYLHGKI IHRDLKPENILNEDMHQIITDGTAKVLSPEKQARAN 240  
Db 181 CTRFYTABIVSALEYLHGKI IHRDLKPENILNEDMHQIITDGTAKVLSPEKQARAN 240  
Qy 241 SFVGTAYQVSPPELLTSACKSSDLWALGCIYQLVGLAPFPAGNEYLIFOKI I KLEYD 300  
Db 241 SFVGTAYQVSPPELLTSACKSSDLWALGCIYQLVGLAPFPAGNEYLIFOKI I KLEYD 300

PT modulate activity of a human ortholog of genes that modify the p53  
PT pathway in Drosophila.  
XX

PS Example 2; Page 439-440; 678pp; English.

XX  
CC The invention relates to identifying (M1) a candidate p53 pathway  
CC modulating agent, by contacting an assay system comprising a purified HM  
CC polypeptide (human orthologue of genes that modify the p53 pathway in  
CC Drosophila) or nucleic acid with a test agent under conditions, where but  
CC for the presence of the test agent, the system provides a reference  
CC activity, and detecting a test agent-biased activity of the assay system.  
CC Also included are modulating (M2) a p53 pathway of a cell (comprising  
CC contacting a cell defective in p53 function with a candidate modulator  
CC that specifically binds to a HM polypeptide comprising an HM amino acid  
CC sequence, where p53 function is restored), modulating (M3) a p53 pathway  
CC in a mammalian cell (comprising contacting the cell with an agent that  
CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)  
CC a disease in a patient (comprising: (a) obtaining a biological sample  
CC from the patient; (b) contacting the sample with a probe for HM  
CC expression; (c) comparing the results with a control; and (d) determining  
CC whether the comparison indicates a likelihood disease). (M1) is useful  
CC for identifying modulators of the p53 pathway. A probe for HM expression  
CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,  
CC in a patient, where the cancer has greater than 25 % expression level.  
CC Modulators identified by (M1) are useful in a variety of diagnostic and  
CC therapeutic applications, where disease or disorder prognosis is related  
CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell  
CC proliferation disorders (e.g. cancer). Another two new methods (M2 and  
CC M3) are useful for modulating the p53 pathway of a cell, thus restoring  
CC the p53 function of the cell, so that the cell undergoes normal  
CC proliferation or progression through the cell cycle. (M2) and (M3) are  
CC also useful for treating defects in the p53 pathway such as angiogenic,  
CC apoptotic or cell proliferation disorders. The present sequence  
XX represents a human p53 pathway modifying protein  
XX

SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLCSCPSPMVRVTSSTPPGPGGSRQGPAMQGTAAEPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSCPSPMVRVTSSTPPGPGGSRQGPAMQGTAAEPRP 60  
Qy 61 GAGSLQHAQPPPPQPKRKPEDPKFKGKILGEGSPSTVVLARELATSREYAIKILEKRII 120  
Db 61 GAGSLQHAQPPPPQPKRKPEDPKFKGKILGEGSPSTVVLARELATSREYAIKILEKRII 120  
Qy 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYPLGSLYAKNGSLKYIKIGSFDET 180  
Db 121 ENKVPVYTRERDVMSRLDHPFFVKLYPTQDDKLYPLGSLYAKNGSLKYIKIGSFDET 180  
Qy 181 CTRFYTABIVSALEYLHGKI IHRDLKPENILNEDMHQIITDGTAKVLSPEKQARAN 240  
Db 181 CTRFYTABIVSALEYLHGKI IHRDLKPENILNEDMHQIITDGTAKVLSPEKQARAN 240



Oy 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
PI |||||  
Db 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKHAFFPESVTWENLHQOTPPKILTA 360  
DB |||||  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKHAFFPESVTWENLHQOTPPKILTA 360  
Oy 361 YLPAMSEDDSDCYGNYDNLISQFGCMQVSSSSSSSLASDGTGLPQRSNGNIQYIHDLD 420  
DB |||||  
Db 361 YLPAMSEDDSDCYGNYDNLISQFGCMQVSSSSSSSLASDGTGLPQRSNGNIQYIHDLD 420  
Oy 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLFARRRQLLLE 480  
DB |||||  
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLFARRRQLLLE 480  
Oy 481 GPHLYYVDPVNKLKGBIPWSQSLRPEAKNFKTFVHTPNRTYYLMDPSGNAHKWCRKIQ 540  
DB |||||  
Db 481 GPHLYYVDPVNKLKGBIPWSQSLRPEAKNFKTFVHTPNRTYYLMDPSGNAHKWCRKIQ 540  
Oy 541 EVWRQRYQSHPDAAVQ 556  
DB |||||  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 7

ABU04708

ID ABU04708 standard; protein; 556 AA.

XX

AC ABU04708;

XX

DT 29-JAN-2003 (first entry)

XX

DE Human expressed protein tag (EPT) #1374.

XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX

OS Homo sapiens.

XX

PN W0200278524-A2.

XX

PD 10-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-US009671.

XX

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX

PA (ZYCO-) ZYCOs INC.

XX

Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKHAFFPESVTWENLHQOTPPKILTA 360  
Oy 361 YLPAMSEDDSDCYGNYDNLISQFGCMQVSSSSSSSLASDGTGLPQRSNGNIQYIHDLD 420  
DB |||||  
Db 361 YLPAMSEDDSDCYGNYDNLISQFGCMQVSSSSSSSLASDGTGLPQRSNGNIQYIHDLD 420  
Oy 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLFARRRQLLLE 480  
DB |||||  
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPMHQFVNNLILQMGVVDKRGKLFARRRQLLLE 480  
Oy 481 GPHLYYVDPVNKLKGBIPWSQSLRPEAKNFKTFVHTPNRTYYLMDPSGNAHKWCRKIQ 540  
DB |||||  
Db 481 GPHLYYVDPVNKLKGBIPWSQSLRPEAKNFKTFVHTPNRTYYLMDPSGNAHKWCRKIQ 540  
Oy 541 EVWRQRYQSHPDAAVQ 556  
DB |||||  
Db 541 EVWRQRYQSHPDAAVQ 556

RESULT 8

ABU04718

ID ABU04718 standard; protein; 556 AA.

XX

AC ABU04718;

XX

DT 29-JAN-2003 (first entry)

XX

DE Human expressed protein tag (EPT) #1384.

XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX

OS Homo sapiens.

XX

PN W0200278524-A2.

XX

PD 10-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-US009671.

XX

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX

PA (ZYCO-) ZYCOs INC.

XX

PI Chicx RM, Tomlinson AJ, Urban RG;

XX

DR WPI; 2003-040607/03.

XX

XX

XX

PI Chicx RM, Tomlinson AJ, Urban RG;

XX

DR WPI; 2003-040607/03.

XX

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

XX

PS Example 2; SEQ ID NO 1374; 134pp; English.

XX

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCPCSPSMVTRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60  
DB |||||  
Db 1 MARTTSQLYDAVPIQSSVVLSCPCSPSMVTRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60  
Oy 61 GAGSLQHAQPPQPPKRGKPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRIIYK 120  
DB |||||  
Db 61 GAGSLQHAQPPQPPKRGKPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRIIYK 120  
Oy 121 ENKVPVYTRERDVMKRLDHPFVKLYPTQDDKLYFGLSYAGKGLLYIKIRKISFDST 180  
DB |||||  
Db 121 ENKVPVYTRERDVMKRLDHPFVKLYPTQDDKLYFGLSYAGKGLLYIKIRKISFDST 180  
Oy 181 CTRFYTAIVSALSYLHGKGIHRDLKPNILNEDMHQIQTDPGTAKVLSPEKQARAN 240  
DB |||||  
Db 181 CTRFYTAIVSALSYLHGKGIHRDLKPNILNEDMHQIQTDPGTAKVLSPEKQARAN 240  
Oy 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
DB |||||  
Db 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKHAFFPESVTWENLHQOTPPKILTA 360

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

XX

PS Example 2; SEQ ID NO 1384; 134pp; English.

XX

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCPCSPSMVTRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60  
DB |||||  
Db 1 MARTTSQLYDAVPIQSSVVLSCPCSPSMVTRTQTSSTPPGIPOGSRQGPAMDQTAAPRP 60  
Oy 61 GAGSLQHAQPPQPPKRGKPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRIIYK 120  
DB |||||  
Db 61 GAGSLQHAQPPQPPKRGKPEDFKFGKILGSGSFSTVVLARELATSREYAIKILEKRIIYK 120  
Oy 121 ENKVPVYTRERDVMKRLDHPFVKLYPTQDDKLYFGLSYAGKGLLYIKIRKISFDST 180  
DB |||||  
Db 121 ENKVPVYTRERDVMKRLDHPFVKLYPTQDDKLYFGLSYAGKGLLYIKIRKISFDST 180  
Oy 181 CTRFYTAIVSALSYLHGKGIHRDLKPNILNEDMHQIQTDPGTAKVLSPEKQARAN 240  
DB |||||  
Db 181 CTRFYTAIVSALSYLHGKGIHRDLKPNILNEDMHQIQTDPGTAKVLSPEKQARAN 240  
Oy 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
DB |||||  
Db 241 SPVGTAGYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Oy 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKHAFFPESVTWENLHQOTPPKILTA 360  
DB |||||  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCESEMGYGLKHAFFPESVTWENLHQOTPPKILTA 360  
Oy 361 YLPAMSEDDSDCYGNYDNLISQFGCMQVSSSSSSSLASDGTGLPQRSNGNIQYIHDLD 420  
DB |||||

Db 361 YLPAMSEDDDCYGNYNLLSQPGCHQVSSSSSSSLASDTGLPQRSGNSIEQYIHDL 420  
XX  
Qy 421 SNSFELDQFSEDEKRLLEKQAGGNPHQPVENNLI LQMGVVDKRGLPARRRQLLLE 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPHQPVENNLI LQMGVVDKRGLPARRRQLLLE 480  
Qy 481 GPHLYYVDPVNKLKGSIPWSQELRPEAKNFKTFVHTPNRTTYLMDPSGNAHKWCRKI 540  
Db 481 GPHLYYVDPVNKLKGSIPWSQELRPEAKNFKTFVHTPNRTTYLMDPSGNAHKWCRKI 540  
Qy 541 EVMRQRYQSHPDAAVQ 556  
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 9

ABU04712  
ID ABU04712 standard; protein; 556 AA.  
XX  
AC ABU04712;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1378.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX

Qy 481 GPHLYYVDPVNKLKGSIPWSQELRPEAKNFKTFVHTPNRTTYLMDPSGNAHKWCRKI 540  
Db 481 GPHLYYVDPVNKLKGSIPWSQELRPEAKNFKTFVHTPNRTTYLMDPSGNAHKWCRKI 540  
Qy 541 EVMRQRYQSHPDAAVQ 556  
Db 541 EVMRQRYQSHPDAAVQ 556

RESULT 10

ABU04716  
ID ABU04716 standard; protein; 556 AA.  
XX  
AC ABU04716;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1382.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1382; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The

PS Example 2; SEQ ID NO 1378; 134pp; English.

XX

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDQTAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDQTAAPRP 60  
Qy 61 GAGSLQHAQPPPPQPRKORPEDFKGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120  
Db 61 GAGSLQHAQPPPPQPRKORPEDFKGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGSLKLYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGSLKLYIRKIGSFDET 180  
Qy 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINLLNEDMHIQITDPTGAKVLSPEKQARAN 240  
Db 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINLLNEDMHIQITDPTGAKVLSPEKQARAN 240  
Qy 241 SPVGTQAYVSPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Db 241 SPVGTQAYVSPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOYGPQKHAFFPESTWENLHQOTPPKLT 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOYGPQKHAFFPESTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCHQVSSSSSSSLASDTGLPQRSGNSIEQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCHQVSSSSSSSLASDTGLPQRSGNSIEQYIHDL 420  
Qy 421 SNSFELDQFSEDEKRLLEKQAGGNPHQPVENNLI LQMGVVDKRGLPARRRQLLLE 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPHQPVENNLI LQMGVVDKRGLPARRRQLLLE 480

CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDQTAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDQTAAPRP 60  
Qy 61 GAGSLQHAQPPPPQPRKORPEDFKGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120  
Db 61 GAGSLQHAQPPPPQPRKORPEDFKGKILGEGSFSTVVLARELATSREYAIKILEKRHIK 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGSLKLYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTQDDSKLYFGLSYAKNGSLKLYIRKIGSFDET 180  
Qy 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINLLNEDMHIQITDPTGAKVLSPEKQARAN 240  
Db 181 CTRFYTABIVSALEYLHGKGIHRDLKPEINLLNEDMHIQITDPTGAKVLSPEKQARAN 240  
Qy 241 SPVGTQAYVSPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Db 241 SPVGTQAYVSPELLTSKACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOYGPQKHAFFPESTWENLHQOTPPKLT 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMBOYGPQKHAFFPESTWENLHQOTPPKLT 360  
Qy 361 YLPAMSEDDDCYGNYNLLSQPGCHQVSSSSSSSLASDTGLPQRSGNSIEQYIHDL 420  
Db 361 YLPAMSEDDDCYGNYNLLSQPGCHQVSSSSSSSLASDTGLPQRSGNSIEQYIHDL 420  
Qy 421 SNSFELDQFSEDEKRLLEKQAGGNPHQPVENNLI LQMGVVDKRGLPARRRQLLLE 480  
Db 421 SNSFELDQFSEDEKRLLEKQAGGNPHQPVENNLI LQMGVVDKRGLPARRRQLLLE 480  
Qy 481 GPHLYYVDPVNKLKGSIPWSQELRPEAKNFKTFVHTPNRTTYLMDPSGNAHKWCRKI 540  
Db 481 GPHLYYVDPVNKLKGSIPWSQELRPEAKNFKTFVHTPNRTTYLMDPSGNAHKWCRKI 540

Oy 541 EVWRORYQSHPDAAVQ 556  
Db 541 EVWRORYQSHPDAAVQ 556

RESULT 11

ABU04711

ID ABU04711 standard; protein; 556 AA.

XX

AC ABU04711;

XX

DT 29-JAN-2003 (first entry)

XX

DE Human expressed protein tag (EPT) #1377.

XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200278524-A2.

XX

PD 10-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-US009671.

XX

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX

PA (ZYCO-) ZYCOs INC.

XX

PI Chicz RM, Tomlinson AJ, Urban RG;

XX

DR WPI; 2003-040607/03.

XX

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

XX

PS Example 2; SEQ ID NO 1377; 134pp; English.

XX

CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 60

Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 60

Oy 61 GAGSLQHAQPPQPKRQKPEDPKFKGKILGEGSFSTVVLARELATSREYAIKILEKRHI1K 120

Db 61 GAGSLQHAQPPQPKRQKPEDPKFKGKILGEGSFSTVVLARELATSREYAIKILEKRHI1K 120

Oy 121 ENKVPVYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180

Db 121 ENKVPVYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180

Oy 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPESSKQARAN 240

Db 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPESSKQARAN 240

Oy 241 SPVGTAAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300

Db 241 SPVGTAAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300

Oy 301 FPEKFFPKARDLVEKLLVLDAIKRLGCEMGGYGLKHAFFPESVTWENLHQTPPKLTA 360

Db 301 FPEKFFPKARDLVEKLLVLDAIKRLGCEMGGYGLKHAFFPESVTWENLHQTPPKLTA 360

Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSSLASDGTLPQSGNSIROYIHDL 420

Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSSLASDGTLPQSGNSIROYIHDL 420

Oy 421 SNSFELDLQFSEDEKRLLEKQAGGNPHQFVBNLLIOMGPDVKRKLFPARRQLLLE 480

Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPHQFVBNLLIOMGPDVKRKLFPARRQLLLE 480

Oy 481 GPHLYYVDPVNKLKGIIPWSQELPBAQNFKTFPVHTPNRTTYLADPSNAHMCCKIK 540

Db 481 GPHLYYVDPVNKLKGIIPWSQELPBAQNFKTFPVHTPNRTTYLADPSNAHMCCKIK 540

Oy 541 EVWRORYQSHPDAAVQ 556

Db 541 EVWRORYQSHPDAAVQ 556

RESULT 12

ABU04706

ID ABU04706 standard; protein; 556 AA.

XX

AC ABU04706;

XX

DT 29-JAN-2003 (first entry)

XX

DE Human expressed protein tag (EPT) #1372.

XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200278524-A2.

XX

PD 10-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-US009671.

XX

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX

PA (ZYCO-) ZYCOs INC.

XX

PI Chicz RM, Tomlinson AJ, Urban RG;

XX

DR WPI; 2003-040607/03.

XX

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

XX

PS Example 2; SEQ ID NO 1372; 134pp; English.

XX

CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 60

Db 1 MARTTSQLYDAVPIQSSVVLSCSPSPMVRTQTESSTPPGIPGSGRQGPAMDGTAAAPRP 60

Oy 61 GAGSLQHAQPPQPKRQKPEDPKFKGKILGEGSFSTVVLARELATSREYAIKILEKRHI1K 120

Db 61 GAGSLQHAQPPQPKRQKPEDPKFKGKILGEGSFSTVVLARELATSREYAIKILEKRHI1K 120

Oy 121 ENKVPVYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180

Db 121 ENKVPVYVTRERDVMSRLDHPFFVKLYPTFQDDKLYFGLSYAKGELLKYIRKIGSFDET 180

Oy 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPESSKQARAN 240

Db 181 CTRFYTABIVSALEYLHGKGIHRLDKPENILLNEDMHIQITDPTAKVLSPESSKQARAN 240

Oy 241 SPVGTAAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300

Db 241 SPVGTAAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300

Oy 301 FPEKFFPKARDLVEKLLVLDAIKRLGCEMGGYGLKHAFFPESVTWENLHQTPPKLTA 360

Db 301 FPEKFFPKARDLVEKLLVLDAIKRLGCEMGGYGLKHAFFPESVTWENLHQTPPKLTA 360

Oy 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSSLASDGTLPQSGNSIROYIHDL 420

Db 361 YLPAMSEDDDCYGNYNLLSQPGCMQVSSSSSSSLASDGTLPQSGNSIROYIHDL 420

Oy 421 SNSFELDLQFSEDEKRLLEKQAGGNPHQFVBNLLIOMGPDVKRKLFPARRQLLLE 480

Db 421 SNSFELDLQFSEDEKRLLEKQAGGNPHQFVBNLLIOMGPDVKRKLFPARRQLLLE 480

Oy 481 GPHLYYVDPVNKLKGIIPWSQELPBAQNFKTFPVHTPNRTTYLADPSNAHMCCKIK 540

Db 481 GPHLYYVDPVNKLKGIIPWSQELPBAQNFKTFPVHTPNRTTYLADPSNAHMCCKIK 540

Oy 541 EVWRORYQSHPDAAVQ 556

Db 541 EVWRORYQSHPDAAVQ 556

RESULT 13

ABU04714

ID ABU04714 standard; protein; 556 AA.

XX

AC ABU04714;

XX  
DT 29-JAN-2003 (first entry)  
XX  
DB Human expressed protein tag (EPT) #1380.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1380; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

5Q Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPMVRTQTESSTPPGIPOGSRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPMVRTQTESSTPPGIPOGSRQGPAMDGTAAAPRP 60  
Qy 61 GAGSLQHAQPPQPQRKRPEDFKFKGILGEGSFSTVVLARELATSREYAIKILEKHH1IK 120  
Db 61 GAGSLQHAQPPQPQRKRPEDFKFKGILGEGSFSTVVLARELATSREYAIKILEKHH1IK 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKGELLKYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKGELLKYIRKIGSFDET 180  
Qy 181 CTRPYTASIVSALEYLHGKIIHRDLKPENILLNEDWHIQTDPGTAKVLSPESSKQARAN 240  
Db 181 CTRPYTASIVSALEYLHGKIIHRDLKPENILLNEDWHIQTDPGTAKVLSPESSKQARAN 240  
Qy 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Db 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMGGYGLKQHPFESVTWNHQQTPPKLTA 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMGGYGLKQHPFESVTWNHQQTPPKLTA 360  
Qy 361 YLPAMSEDDDCYGNVDNLLSQPGCHQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420  
Db 361 YLPAMSEDDDCYGNVDNLLSQPGCHQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420  
Qy 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGPVDKRGLFARRRQLLLTE 480  
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGPVDKRGLFARRRQLLLTE 480  
Qy 481 GPHLYYVDPVNKLKGSIPWSQLRPEANFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540  
Db 481 GPHLYYVDPVNKLKGSIPWSQLRPEANFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540  
Qy 541 EVWRQRYQSHDAAVQ 556  
Db 541 EVWRQRYQSHDAAVQ 556

RESULT 14  
ABU04707  
ID ABU04707 standard; protein; 556 AA.  
XX  
AC ABU04707;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1373.  
XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1373; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

Qy 1 MARTTSQLYDAVPIQSSVVLCSGPCSPMVRTQTESSTPPGIPOGSRQGPAMDGTAAAPRP 60  
Db 1 MARTTSQLYDAVPIQSSVVLCSGPCSPMVRTQTESSTPPGIPOGSRQGPAMDGTAAAPRP 60  
Qy 61 GAGSLQHAQPPQPQRKRPEDFKFKGILGEGSFSTVVLARELATSREYAIKILEKHH1IK 120  
Db 61 GAGSLQHAQPPQPQRKRPEDFKFKGILGEGSFSTVVLARELATSREYAIKILEKHH1IK 120  
Qy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKGELLKYIRKIGSFDET 180  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYAKGELLKYIRKIGSFDET 180  
Qy 181 CTRPYTASIVSALEYLHGKIIHRDLKPENILLNEDWHIQTDPGTAKVLSPESSKQARAN 240  
Db 181 CTRPYTASIVSALEYLHGKIIHRDLKPENILLNEDWHIQTDPGTAKVLSPESSKQARAN 240  
Qy 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Db 241 SPVGTQAYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIPOKIKLEYD 300  
Qy 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMGGYGLKQHPFESVTWNHQQTPPKLTA 360  
Db 301 FPEKFFPKARDLVEKLLVLDATKRLGCEMGGYGLKQHPFESVTWNHQQTPPKLTA 360  
Qy 361 YLPAMSEDDDCYGNVDNLLSQPGCHQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420  
Db 361 YLPAMSEDDDCYGNVDNLLSQPGCHQVSSSSSHLSASDTGLPQRSGSNIEQYIHDL 420  
Qy 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGPVDKRGLFARRRQLLLTE 480  
Db 421 SNSFELDLPSEDEKRLLEKQAGGNPWHQPVNNLLKMGPVDKRGLFARRRQLLLTE 480  
Qy 481 GPHLYYVDPVNKLKGSIPWSQLRPEANFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540  
Db 481 GPHLYYVDPVNKLKGSIPWSQLRPEANFKTFPVHTPNRTYYLMDPSNAHWCRIQ 540  
Qy 541 EVWRQRYQSHDAAVQ 556  
Db 541 EVWRQRYQSHDAAVQ 556

RESULT 15  
ABU04717  
ID ABU04717 standard; protein; 556 AA.  
XX  
AC ABU04717;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1383.  
XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCO S INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1383; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 556 AA;

Query Match 100.0%; Score 2941; DB 6; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.3e-249;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRVTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60  
|||||  
Db 1 MARTTSQLYDAVPIQSSVVLCSPPSPMVRVTQTESSTPPGIPGSGRQGPAMDGTAAEPRP 60

Oy 61 GAGSLQHAQPPQPFRKKRPEDPKFKILQSGSPSTVVLARELATSREYA I KILSKRH I I K 120  
|||||  
Db 61 GAGSLQHAQPPQPFRKKRPEDPKFKILQSGSPSTVVLARELATSREYA I KILSKRH I I K 120  
Oy 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYANGHELLKY I RKIGSPDET 180  
|||||  
Db 121 ENKVPYVTRERDVMSRLDHPFFVKLYPTFQDDSKLYPGLSYANGHELLKY I RKIGSPDET 180  
Oy 181 CTRPYTASIVSALEYLHGKDI I HRDLKPEN I LLNEDMGH I Q I TDPGTAKVLSPEKQARAN 240  
|||||  
Db 181 CTRPYTASIVSALEYLHGKDI I HRDLKPEN I LLNEDMGH I Q I TDPGTAKVLSPEKQARAN 240  
Oy 241 SFVGTAGVVSPELLTEKSACKSSDLWALGCI I YQLVAGLPPFRAGNEYL I PKI I KLEYD 300  
|||||  
Db 241 SFVGTAGVVSPELLTEKSACKSSDLWALGCI I YQLVAGLPPFRAGNEYL I PKI I KLEYD 300  
Oy 301 FPEKFFPKARDLVEKLLVLDATIKRLGCSMEQGYPLQHPFFPSVTWENLHOOTPPKLT A 360  
|||||  
Db 301 FPEKFFPKARDLVEKLLVLDATIKRLGCSMEQGYPLQHPFFPSVTWENLHOOTPPKLT A 360  
Oy 361 YLPAMSEDDDCYQNYDNLLSQFGCHQVSSSSSHSLASDGTGLPQRSQSNIEQY I HDLD 420  
|||||  
Db 361 YLPAMSEDDDCYQNYDNLLSQFGCHQVSSSSSHSLASDGTGLPQRSQSNIEQY I HDLD 420  
Oy 421 SNSFELDLPSEDSKRLLLSKQAGGNPMHQPVENNL I LKQGVDKRKLFAARRQLLLT E 480  
|||||  
Db 421 SNSFELDLPSEDSKRLLLSKQAGGNPMHQPVENNL I LKQGVDKRKLFAARRQLLLT E 480  
Oy 481 GPHLYYVDPVNKVLKGEI PWSQLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540  
|||||  
Db 481 GPHLYYVDPVNKVLKGEI PWSQLRPEAKNFKTFPVHTPNRTTYLMDPSGNAHWCKRIQ 540  
Oy 541 EVWRQRYQSHPDAAVQ 556  
|||||  
Db 541 EVWRQRYQSHPDAAVQ 556

Search completed: June 27, 2006, 01:31:14  
Job time : 199 secs

OM protein - protein search, using sw model

Run on: June 27, 2006, 01:31:32 ; Search time 42 Seconds  
(without alignments)  
1273.727 Million cell updates/sec

Title: US-10-689-576-1  
Perfect score: 2941  
Sequence: 1 MARITTSQLYDAVPIQSSVVL.....RKIQSVWRQYQSHPDAAVQ 556

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Match	Length	DB ID	Description
1	873.5	29.7	592	2 T43402	probable protein k
2	832	28.3	488	2 T48447	3-phosphoinositide
3	748.5	25.5	1081	2 S51899	probable protein k
4	733	24.9	550	2 T40486	phosphoinositide-d
5	712	24.2	766	2 S69657	hypothetical prote
6	648.5	22.1	898	2 S69634	hypothetical prote
7	606.5	20.6	893	2 S63378	hypothetical prote
8	568.5	19.3	648	1 JQ1150	protein kinase (EC
9	566	19.2	471	2 S68463	protein kinase ATP
10	565.5	19.2	320	2 T33662	hypothetical prote
11	565.5	19.2	465	2 S68462	protein kinase ATP
12	562.5	19.1	431	2 A48094	serum and glucocor
13	561.5	19.1	338	2 S00085	protein kinase (EC

A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-592 <WOO>  
A;Cross-references: UNIPARC:UPI0000069B00; EMBL:AL031798; PIDN:CAA21194.1;  
GSPDB:GNO0068; SPDB:SPCC576.15c  
A;Experimental source: strain 972h-; cosmid c576  
C;Genetics:  
A;Gene: KSG1; SPCC576.15c  
A;Map position: 3  
A;Introns: 191/3  
C;Keywords: phosphotransferase

Query Match 29.7%; Score 873.5; DB 2; Length 592;  
Best Local Similarity 37.3%; Pred. No. 1.3e-29;  
Matches 212; Conservative 89; Mismatches 166; Indels 101; Gaps 17;

Qy	14	IQSSVVLCSPPSMVVRQTTSSTPPGIPGSRQGFAMDTAASPRGAGSLQHAQPPPP 73
Db	49	IPQSNALATTTPNESTQSDISSPKIPSAVP-----HISTPNPSSGA-----ST 90
Qy	74	PRKQRPEDFKFGKILGSGSFSTVVLARSLATSRYSIAIKILEKRIIIEKNKVPVYTRERDV 133
Db	91	PHIKRVSDPKFGSILGEGSYSTVLATENSTKREYAIKVLQKHIIKEKKEKYVNIKEA 150
Qy	134	MSRLD-HPPFVKLYPTFQDDKLYPGLSYAKNGELLYKIRKIGSPDETCTRTFYATIRVSA 192
Db	151	LCILSKHPGFKLFTTFQDAHNLVYVLSLARGSLLODYINKLGRFNBICAQYAAALIVDS 210
Qy	193	LEYLHGKGIHRLDKPENILLNEDHGIQITDPTAKVLS-----PESKQARAN 270
Db	211	IDYHGRGVIRHDLKPENILLNEDHGIQITDPTAKVLS-----PESKQARAN 270
Qy	241	SFVGTAAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPFPFRAGNYLIPKIKILEYD 300
Db	271	SFVGTARYVSPVLSLKIAGTASDIWARGCILFQMLAGKPPFVAGNYLTPQSIHLHLYE 330
Qy	301	PPSKFPFKARDLVEKLLVLDATKRLGCEBMOYGPPLKHAHPFESVTWEN-LHQTPPKILT 359
Db	331	IPPDISDVASDLIKGLVLDPKDLTVDE-----LHGFPPGKIFDNTLWELPPRLK 384
Qy	360	AYLPAMSEDDSDCYGNVNDLLSGPQGVSSSSSSSS-----LSASDTGLQ 406
Db	385	PP-----GHTSVLS-----LSVPAASHHKGDLTSLPLGVPMKVSASTNAAPS 427
Qy	407	RSGSNIEQYIHLDLNSNPFELQFS-----EDSK-----RLLEKQAG--GNPWHOPVENN 455
Db	428	PVOTFNRTGLLPCQSNLEBENKSSSILQDDSKIISKIOTLVNYSMSGINGNDAPRPPFS- 486
Qy	456	LILHMGVVDKRLGFLARR--RQLLLTS-GPHLYYVD--PWNKVLKGISP--MSQELRPE 507
Db	487	-----LPRKIKRPTFILTNGRYLCVADGGRKRVKESIPKSVQMRKRV 533
Qy	508	AKNFKTFPVHTPHRTTYLWDPGSAHGW 535
Db	534	KNNHGHVVTPTKSSSFEDPNGPASAW 561

14	560.5	19.1	358	2 T38121	protein kinase - h
15	558.5	19.0	351	1 OKHYCB	protein kinase (EC
16	558.5	19.0	351	1 OKHYCB	protein kinase (EC
17	558.5	19.0	351	1 OKHYCB	protein kinase (EC
18	558.5	19.0	425	2 S41099	protein kinase (EC
19	557.5	19.0	351	1 OKBOB1	protein kinase (EC
20	557.5	19.0	371	2 T16391	hypothetical prote
21	557.5	19.0	397	1 OKBOB2	protein kinase (EC
22	557	18.9	334	2 A60543	protein kinase (EC
23	556	18.9	398	1 OKBYC3	protein kinase (EC
24	555	18.9	680	2 S37955	protein kinase YPK
25	554	18.8	380	1 OKBYC2	protein kinase (EC
26	552	18.8	502	2 F31751	protein kinase cat
27	550.5	18.7	351	1 OKHYCB	protein kinase (EC
28	548.5	18.7	312	2 T32446	hypothetical prote
29	548.5	18.7	312	2 A29460	protein H42K2.1 [
30	548	18.6	375	2 T21212	hypothetical prote
31	547.5	18.6	726	2 S22258	probable protein k
32	546.5	18.6	677	2 JS0178	protein kinase YKR
33	546	18.6	351	1 OKBO2C	protein kinase (EC
34	545.5	18.5	1092	2 H96509	protein F27F5.23 [
35	544.5	18.5	360	1 OKHUCG	protein kinase (EC
36	543	18.5	359	2 T21211	hypothetical prote
37	542	18.4	351	1 OKHUC2	protein kinase (EC
38	541	18.4	351	1 OKHYCA	protein kinase (EC
39	541	18.4	375	1 OKHUC2	protein kinase (EC
40	540.5	18.4	569	2 T50414	probable prolifera
41	539.5	18.3	479	2 A38578	protein kinase 2 (
42	539.5	18.3	541	1 T43232	protein kinase (EC
43	538	18.3	351	1 OKM5CA	protein kinase (EC
44	538	18.3	480	2 S56639	ribosomal protein
45	537	18.3	351	1 OKRT2C	protein kinase (EC

ALIGNMENTS

RESULT 1

T43402  
probable protein kinase (EC 2.7.1.-) - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: *Schizosaccharomyces pombe*  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43402; T41425  
R;Niederberger, C.  
submitted to the EMBL Data Library, July 1998  
A;Reference number: Z22486  
A;Accession: T43402  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-592 <NIE>  
A;Cross-references: UNIPROT:Q12701; UNIPARC:UPI0000069B00; EMBL:X99280;  
PIDN:CAA67672.1  
A;Experimental source: strain h90  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, September 1998  
A;Reference number: Z21954  
A;Accession: T41425

RESULT 2

T48447  
3-phosphoinositide-dependent protein kinase-1 PDK1 - *Arabidopsis thaliana*  
N;Alternate names: protein T32M21.110  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48447  
R;Bevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De Keyser, A.; Neyt, P.; Rouse, P.; Van Den Daele, H.; Villarroel, R.; Gielen, J.; Van Montagu, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24487  
A;Accession: T48447  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-488 <BEV>  
A;Cross-references: UNIPROT:Q9LZ74; UNIPARC:UPI000009C594; EMBL:AL162875  
A;Experimental source: cultivar Columbia; BAC clone T32M21  
C;Genetics:  
A;Map position: 5  
A;Introns: 54/3; 115/1; 132/3; 166/3; 203/1; 229/2; 284/3; 329/3; 387/2; 461/3  
A;Note: T32M21.110

Query Match 28.3%; Score 832; DB 2; Length 488;  
Best Local Similarity 40.2%; Pred. No. 5.6e-28;  
Matches 192; Conservative 69; Mismatches 165; Indels 52; Gaps 11;

Qy	81	DPKPGKILGSGSFSTVVLARSLATSRYSIAIKILEKRIIIEKNKVPVYTRERDVMSKRLDHP 140
Db	40	DFSPGKIYGVGSRVRAKRGSTOTVYALKMDKXPIKENTATVVLERIVLDQLSHP 99
Qy	141	FPVKLYPTFQDDKLYPGLSYAKNGELLYKIRKIGSPDETCTRTFYATIRVSAVLYHGKQ 200
Db	100	QIKLYPTFQDTSLLYALSCGSGELPDQITKGRGLSEDEARPYTARVVDALYHISWG 159
Qy	201	IIRDLKPENILLNEDHGIQITDPTAKVLS-----VLSPEKQARANSFVGTAAQYVSP 252
Db	160	IIRDLKPENILLNEDHGIQITDPTAKVLS-----VLSPEKQARANSFVGTAAQYVSP 219
Qy	253	LLEKSACKSSDLWALGCIYQLVAGLPFPFRAGNYLIPKIKILEYDFFPKFPKARDL 312
Db	220	VLNSSPATFGNDLWALGCTLYQKLSQTSPPKASDWLPQRIIARDIKFNPSPSAARDL 279
Qy	313	VEKLLVLDATKRLGCEBMOYGPPLKHAHPFESVTWENLHQTPPKILTAYLPA---MSDD 369
Db	280	IDRLDTPSPRRPGAGS-EGYVALKRRHPPKRVQVWNLRSQTPPKL-ADPAGSATSPER 337
Qy	370	EDCYGNVNDLLSGPQGVSSSSSSSS-----LSASDTGLPQSGNSNIEQYIHLDLNSNPFEL 426
Db	338	DTGHSFVN-LTHIG-DSLATNGHGSAPPFSSSSSSSITRLAS-----IDSPDSR--- 386
Qy	427	DLQPSDEKRLLEKQAGNPNHQPVE-NHLLHMGVVDKRLGFLARRRQLLTETPHLY 485
Db	387	-----WQPLSPGRSVLNIQAVIKLQIKTSKKVQLILTNPKIL 425
Qy	486	YVDPVNVKLGKIPW---SQSLRPAKQFTFPVHTPHRTTYLWDPGSAHMKKIQ 540

Db 426 YVDPFKLVVKGNIIMSDNSDLAVVVTSPSHFICTPKKVLSPDAKQASVMGGAIE 483

### RESULT 3

S51899

probable protein kinase HRC1081 (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: protein Q0784; protein YOL100w  
C:Species: *Saccharomyces cerevisiae*  
C>Date: 05-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 05-Oct-2004  
C:Accession: S51899; S59175; S66796  
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.  
submitted to the EMBL Data Library, January 1995  
A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV  
including the Ty1-H3 retrotransposon, the *sufl1(+)* frameshift suppressor gene for  
tRNA-Gly, the yeast transfer RNA-Thr-1a and a Delta.  
A:Reference number: S51848  
A:Accession: S51899  
A:Molecule type: DNA  
A:Residues: 1-1081 <VAN>  
A:Cross-references: UNIPROT:Q12236; UNIPARC:UP1000004F9FC; EMBL:Z48149;  
NID:g663234; PIDN:CAA88162.1; PID:g663254  
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.  
Yeast 11, 1069-1075, 1995  
A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV  
including the Ty1-H3 retrotransposon, the *sufl1(+)* frameshift suppressor gene for  
tRNA-Gly, the yeast transfer RNA-Thr-1a and a delta element.  
A:Reference number: S59156; MUID:96076631; PMID:7502582  
A:Accession: S59175  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1081 <VAN>  
A:Cross-references: UNIPARC:UP1000004F9FC; EMBL:Z48149; NID:g663234;  
PIDN:CAA88162.1; PID:g663254  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January  
1995  
R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S66791  
A:Accession: S66796  
A:Molecule type: DNA  
A:Residues: 1-1081 <DUR>  
A:Cross-references: UNIPARC:UP1000004F9FC; EMBL:Z74842; NID:g1419951;  
PIDN:CAA99113.1; PID:e251892; PID:g1419952; MIPS:YOL100w  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:PKH2  
A:Cross-references: SGD:S0005460  
A:Map position: 15L  
C:Keywords: ATP; phosphotransferase  
P:177-443/Domain: protein kinase homology <KIN>  
P:185-193/Region: protein kinase ATP-binding motif

Query Match 25.5%; Score 748.5; DB 2; Length 1081;  
Best Local Similarity 38.1%; Pred. No. 3.2e-24;  
Matches 164; Conservative 79; Mismatches 109; Indels 79; Gaps 11;

A:Cross-references: UNIPARC:UP1000006A777; EMBL:AL049489; PIDN:CA39805.1;  
GSPDB:GN00067; SPDB:SPBC1778.10c  
A:Experimental source: strain 972h-; cosmid c1778  
C:Genetics:  
A:Gene: SPBC4C3.11; SPDB:SPBC1778.10c  
A:Map position: 2  
C:Keywords: phosphotransferase

Query Match 24.9%; Score 733; DB 2; Length 550;  
Best Local Similarity 36.4%; Pred. No. 7.7e-24;  
Matches 185; Conservative 82; Mismatches 165; Indels 76; Gaps 16;

Qy 77 KRPEDFKGKILGSGSFSTVVLARELATSREYAIKILEKHIIKENKVPVYTRERDVMS 136  
Db 49 KSPADYVPGDIIGDGSFKVRRATDKGSKGYAIKVLKIKYIVKENKVKYVNIERDSMOR 108

Qy 137 LD-HPPFVKLYPTFQDDSKLYGLSYAKGGLKLYIRKIGSPDSTCTRPYTAISVSALEY 195  
Db 109 LMGFPGISRLFTFQDDSKLYGLSYAKGGLKLYIRKIGSPDSTCTRPYTAISVSALEY 168

Qy 196 LHGKGIHRLDKPENILLNEDMHQIQTDPOTAKVLSPEKQAR-----ANSFVGTAYQVVS 250  
Db 169 MHSOGIHRDLKPENILFDGNGHIVKIDTDPOTAKILPPKYVNSPDYTFPSSFVGTAYVA 228

Qy 251 PELLTEKSACKSSDDLWALGCIYYVLVAGLPPFRAGNEYLIPOKIIKLEYDFPEKFPKAR 310  
Db 229 PELLRSQVVSCKSSDDLWAFACVYQIMVGSPPPHOSNPNIFKKIMSELYSLPKLLPPDIV 288

Qy 311 DLVEKLLVLDATKRLGCESEMGYGLPKAHPPFESVTWENLHQTPPKLTAYLPAMSEDDR 370  
Db 289 PLPSHLFRIQPSDRSTTQO-----IKOPFFATITWDLNLTQDPFPMSFRP----- 335

Qy 371 DCYGYND-----NLLSGQFCQVSSSSSSSHLSASDTGLP--QRS 408  
Db 336 ----NYNIAIPNAPYRSNVTAAAAAANAAP-----ASAVIGHQETARRQELPTVNR 387

Qy 409 GSNIRQYIH-DLDSNSFELDQFSE--DBKRLLEKQAQGNPHQFVNNLILKMGVPD 464  
Db 388 TAPTAHYGASLSRQMPVDRILYKLVPSSESIESTSVFVSPIPSVPGQVQV---PSQ 443

Qy 465 KRKGLFARRRQ--LLLT-----GPH--LYYDVVNVKVLKGIIPWSQSLRPAKQV 511  
Db 444 LSK-MFLKQKQVRLMLTGVGRCAFCVKQKHEFLFIEGVN--LKDS--SVVVIPDENSS 497

Qy 512 KTFPVHTPNRTYLLADPSGNHAKHCKKI 539  
Db 498 KRFLIEDKQVSWIIEDSSGDVTKYDKKI 525

### RESULT 5

S69657

hypothetical protein YDR490c - yeast (*Saccharomyces cerevisiae*)  
C:Species: *Saccharomyces cerevisiae*  
C>Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 05-Oct-2004  
C:Accession: S69657  
R:Dietrich, F.S.  
submitted to the EMBL Data Library, August 1995

Qy 76 KCRPDKFKGKILGSGSFSTVVLARELATSREYAIKILEKHIIKENKVPVYTRERDVMS 135  
Db 173 KKGIDKDFKQSGVIGGAYSTVHLATSIDTQKRAAKVHLKSEYLRQKVKYVSISATLQ 232

Qy 196 RLQH-PPFVKLYPTFQDDSKLYGLSYAKGGLKLYIRKIGSPDSTCTRPYTAISVSALEY 194  
Db 233 KLNNSPVSRLFTFQDDSSLYFLLEYAFNKGDFLIMKQKYLKQKYLKQKYLKQKYLKQKYL 292

Qy 195 YLHGKGIHRLDKPENILLNEDMHQIQTDPOTAKVLSPEKQAR-----QARANSFVGT 245  
Db 293 YLHSGIHRDLKPENILLDGBMKIKLTDPTAKLNPNTNSVSKPEYDLSTRSKSPVOT 352

Qy 246 AQYVPELLTEKSACKSSDDLWALGCIYYVLVAGLPPFRAGNEYLIPOKIIKLEYDFPEKFP 305  
Db 353 ASYVSPSELLDSDPTDYRCIDMAPGCIILFQMIAGKPPFKATHSYLTPOKVMKQVAFTPGF 412

Qy 306 FPKARDLVKLLVLDATKRLGCESEMGYGLPKAHPPFESVTWENLHQTPPKLTAYLPAMSE 362  
Db 413 PLIIRDLVKKILVKNLDRRLTISQ-----IKEHFFKDLNFKDGSVMSKTPPEIKPYKI 466

Qy 363 PAMSEDDDCYKYNIDNLSQFGQVSSSSSHLSASDTGLPQRSGS--NIR 413  
Db 467 NAKS-----MQAMPQSGDKLVKQSVNTLQKSHLVTRQSASSPSVB 507

Qy 414 QYIHDLDSNSFELDQFSEDBKRLLEKQAQGNPHQFVNNLILKMGVPD----- 465  
Db 508 ETTHTSTLYN-----NHTASTSEISIKRPTDSRTAQILEN 544

Qy 466 -RKGLFARRRQ 475  
Db 545 ARKQINNRRKQ 555

### RESULT 4

T40486

phosphoinositide-dependent protein kinase 1 (EC 2.7.1.-) SPBC4C3.11 (imported) -  
fission yeast (*Schizosaccharomyces pombe*)  
C:Species: *Schizosaccharomyces pombe*  
C>Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C:Accession: T40486; T39692  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.;  
Dueterhoeft, A.  
submitted to the EMBL Data Library, February 1998  
A:Reference number: Z21910  
A:Accession: T40486  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-420 <KOO>  
A:Cross-references: UNIPROT:Q9Y7J6; UNIPARC:UP10000069850; EMBL:AL021730;  
PIDN:CAA16833.1; GSPDB:GN00067; SPDB:SPBC4C3.11  
R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, March 1998  
A:Reference number: Z21869  
A:Accession: T39692  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 385-550 <OLI>

A:Description: The sequence of *S. cerevisiae* cosmid 9410, 8035, 8166, and 9787.  
A:Reference number: S69554  
A:Accession: S69557  
A:Molecule type: DNA  
A:Residues: 1-766 <DIE>  
A:Cross-references: UNIPROT:Q03407; UNIPARC:UP1000006A3C7; EMBL:U33050;  
NID:g92726; PIDN:AAB64917.1; PID:g927745; MIPS:YDR490c  
C:Genetics:  
A:Gene: SGD:PKH1  
A:Cross-references: SGD:S0002898  
A:Map position: 4R  
C:Keywords: ATP  
P:123-391/Domain: protein kinase homology <KIN>  
P:131-139/Region: protein kinase ATP-binding motif

Query Match 24.2%; Score 712; DB 2; Length 766;  
Best Local Similarity 30.3%; Pred. No. 7.7e-23;  
Matches 187; Conservative 87; Mismatches 154; Indels 190; Gaps 15;

Qy 27 SMVKTQTESSTPPGIPGSGRQ-----PMDGT-----AASPRGAGSLQH 67  
Db 22 SAETHTQGYPRFVVDGNSNSQSGSELAQSPQGFGLKSTNRPILANDPQ-----MQH 78

Qy 68 AQP-PPQPRKQKPE-----DFKFGKILGSGSFST 95  
Db 79 EMGLDPSMRRRRRBNASGAAKIVQDVDPATGLTGHVVIQIKDFPGEGLDQSGYS 138

Qy 96 VLARELATSREYAIKILEKHIIKENKVPVYTRERDVMSRLDHPFFV-KLYPTFQDDSK 154  
Db 139 VVLATARDSCKYAKVLSKYLIRQKVKYVTVKGLALQKNGTQIFGLPFTQDSAS 198

Qy 155 LYGLSYAKGGLKLYIRKIGSPDSTCTRPYTAISVSALEYLHGKGIHRLDKPENILLN 214  
Db 199 YFLLEYAPHGDPLGLIKYKYSLNSTCARYTAQSIDAVDSLWNIQIHRDLKPENILLD 258

Qy 215 EDKHIQTDPOTAKVLSPEKQ-----ARANSFVGTAYQVPELLTEKSACKSS 263  
Db 259 KMKVKLTDPTAKILPESPENTADKPYDYLAQSKSPVGTATYVPELLANDNYDSRC 318

Qy 264 DLWALGCIYYVLVAGLPPFRAGNEYLIPOKIIKLEYDFPEKFPKARDLVKLLVLDATK 373  
Db 319 DIMAFGCIYQKLAGKPPFKAAYEYLTPOKVKIYQVAFYAGPPQIVKDLVKKLVDPND 328

Qy 324 RLCESEMGYGLPKAHPPFESVTWENLHQTPPKLTAYLPAMSEDD- 369  
Db 379 RLTIKQ-----IKAHLPFHEVNFEDGSVMDNPPRIOPYKINAEAMQLQVSESDTTV 432

Qy 370 -----EDC 372  
Db 433 KMANLQLAGKHADTPLQAPATSGEHSVISMATAATAPNKDYTSQPKLKSSTSVRSA 492

Qy 373 YGVYDNLSSQFGQVSSSSSHLSASDTGLPQRSGS--IEQYIHDLDSNSFELDQ 429  
Db 493 SNNTDRBVIQKVKSNRASVSSPISSTTRGKDNKRSSEDAFNSRVLQND----- 543

Qy 430 FSEDBKRLLEKQAQ-----GNPHQFVNNLILKMGVPDKKQL 469  
Db 498 KRFLIEDKQVSWIIEDSSGDVTKYDKKI 525



```
Qy      407 RSGSNIEQYI-----HDLDSNSPELOLQPSDEK 435
          || || | | | | | | | | | | | | | | | |
Db      325 ----NIPONILPTROLHVIDTPARSIOITKOKKK 355
```

**RESULT 6**

S69634  
hypothetical protein YDR466w - yeast (*Saccharomyces cerevisiae*)  
C:Species: *Saccharomyces cerevisiae*  
C:Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 05-Oct-2004  
C:Accession: S69634  
R:Dieterich, F.S.  
submitted to the EMBL Data Library, August 1995  
A:Description: The sequence of *S. cerevisiae* cosmid 9410, 8035, 8166, and 9707.  
A:Reference number: S69554  
A:Accession: S69634  
A:Molecule type: DNA  
A:Residues: 1-998 <IDE>  
A:Cross-references: UNIPROT:Q03306; UNIPARC:UP1000006C128; EMBL:U33050;  
NID:g927726; PIDN:AAB64902.1; PID:g927730; MIPS:YDR466w  
C:Genetics:  
A:Cross-references: SGD:S0002874  
A:Map position: 4R  
C:Keywords: ATP  
F:9-293/Domain: protein kinase homology <KIN>  
F:17-25/Region: protein kinase ATP-binding motif

Query Match 22.1%; Score 648.5; DB 2; Length 898;  
Best Local Similarity 37.7%; Pred. No. 3.8e-20;  
Matches 149; Conservative 60; Mismatches 109; Indels 77; Gaps 10;

```

Qy      75  RKRRPDEPKFKGLGGSSYTVLVLAR-LATSREYAKIKLEKRIHKKGNVPYVTRFRDV 133
Db      4  RKRSPHDFIPKESLGHGSSYSTVKALDKKSPNKIYAKVKCSKGIHKEAKVYVYTIKQRT 63

Qy     134  MSRL---DHPFFVKLYPTFGDEKLYPGLSYAJONGELLYIKRKIGSFDETCTFRFYTAIV 190
Db     64  MQLLAQKHAGIKIKYPTFDESNELVPLDPAFGKGLSLHNGQTFDVIWTRHFTAL 123

Qy     191  SAELEYAKRIIHRLDKPLNINLENDHGIITDPTGATKSLV---SSKQKRA 199
Db     71  SAELEYAKRIIHRLDKPLNINLENDHGIITDPTGATKSLV---SSKQKRA 123

Qy     192  DALEFISHIGIIHRLDKPLNINLENDHGIITDPTGAAATIDPSLSDSAKFNDSNGSKGD 183
Db     72  DALEFISHIGIIHRLDKPLNINLENDHGIITDPTGAAATIDPSLSDSAKFNDSNGSKGD 183

Qy     240  N----SPVGTQATVSPPELLTEKSACKSSDLWALGCIITQVLVAGLPDFRAGNSTYLIPQKI 295
Db     184  NQNCASPVGTATVSPPELLTNQCCYGGSDINWALGCIITQVVGQGGPPFRGNELATFEKIV 243

Qy     296  KLEYDP-----PSKFPFKARDVKEKLLVDATKRLGCESEHGQYGLPKHPPFSFVT 346
Db     244  ALDYPMGPNRNINNSTPINFPLVINLWQKILVIVENRILEG-----IKRPFYSKD 297

Qy     347  WENLHQQTTPPKLAYLPMASDEDDCYGNVNLDSQFCQVSSSSSSHLSASDTGLPD 406
Db     298  WNLHQQTTPPKLAYLPMASDEDDCYGNVNLDSQFCQVSSSSSSHLSASDTGLPD 406

Qy     348  WN-----DKIKIRWIIQW-----SQGQSLOOTLNLPL 394

```

Query Match 20.6%; Score 606.5; DB 2; Length 893;  
Best Local Similarity 31.7%; Pred. No. 2e-18;  
Matches 155; Conservative 73; Mismatches 156; Indels 105; Gaps 14;

Qy	20	LCSCPSPP---SKVRTTSTSTTPPGI PGGSRGQGPMQDGTAAEPFGAGSLQIAQPP---P	72
Db	421	LASATSPSSSARKTSGSSNINDKI PGGS-----VFPNNSFFPQSPSPKISDPP	469
Qy	73	QPRKKI-----PDPKFGKILGBGSFSTVLARELATSREYAIKILSK	115
Db	470	EPKRSRLRKTSPSNKPGDIIMVGPSPSKILRLGGQDVGKVLVREKKNINVTALVKLSK	529
Qy	116	RHIIKENKVPVYTRDVRMSRLDHPFKVYPTFDGKVLGSLYAGSLKKLYI---RK	173
Db	530	DEMIRKNNIKRVLTQSILATSNHPIVTLVYHSGSDYLVLCKYCHGSGFPRALQTRK	589
Qy	174	IGSFDTCTCTPTTASIVSALEYLHGKGI IHRDLKPENILINEDWHQITDP-----	224
Db	590	TKCI CEDDARPTASVEALVAYLHLGPI YRDLKPNILHQSQSHILSDPDLISIQAKDS	649
Qy	225	-----GTAKVLSPSKQA-----RANSFVGTQAQVSPBLTETKSACKSSDLWALGCI IYQ	274
Db	650	KVPVVGSKAQSTLVDTKICSDGFRTNSPVGTESYIAPEVIRKNGHTAAVDNMTGLI IYE	709
Qy	275	LVAGLPFPFRAGNEYILPQKI IKLKYDPP---SKFFPKARDLVEKLVLVDATKRLGCSMEIG	332
Db	710	MLPQPLTPGQMDKNTNTHPI LQGVSPFNPNISIPSTCDITKGLTNLSSGSLGCKG---KG	767
Qy	333	YQPLKAPFPFSSVETWNLKQDTPPKLTYLTPMAGSDSDCYQGNVLDNLSQGPQVSSSS	399

**RESULT 8**

JQ1150  
 protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold  
 (Dictyostelium discoideum)  
 C:Species: Dictyostelium discoideum  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C:Accession: JQ1150  
 R:Buerki, S.; Anjard, C.; Scholder, J.C.; Raymond, C.D.  
 Gene 102, 57-65, 1991  
 A:Title: Isolation of two genes encoding putative protein kinases regulated  
 during Dictyostelium discoideum development.  
 A:Reference number: JQ1150; MUID:91323730; PMID:1864510  
 A:Accession: JQ1150  
 A:Molecule type: DNA  
 A:Residues: 1-648 #EUS#  
 A:Cross-references: UNIPROT:P34099; UNIPARC:UPI000012DC1F; GB:M38703  
 C:Genetics:  
 A:Gene: PK2  
 A:Introns: 578/3  
 C:Complex: heterodimer with regulatory chain; active catalytic chain is released  
 when cAMP binds to the regulatory chain  
 C:Function:  
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-  
 threonine-phosphate using ATP  
 A:Note: important for cell type differentiation and fruiting body morphogenesis  
 C:Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain;  
 protein kinase homology  
 C:Keywords: ATP; magnesium; phosphoprotein; phosphotransferase;  
 serine/threonine-specific protein kinase  
 F:136-223/Region: glutamine-rich  
 F:297-312/Region: glutamine-rich  
 F:134-590/Domain: protein kinase homology cKIN#  
 F:142-350/Region: protein kinase ATP-binding motif  
 F:165,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:464,468/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 19.3%; Score 568.5; DB 1; Length 648;  
Best Local Similarity 36.7%; Pred. No. 5.7e-17;  
Matches 115: Conservative 68: Mismatches 113: Indels 17: Gaps 4:

[illegible]

## RESULT 9

568463  
protein kinase ATPK19 (SC 2.7.1.-) - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 05-Dec-1996 #sequence\_revision 27-Feb-1997 #tax\_change 05-Oct-2004  
C/Accession: 568463  
R/Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.  
PDBS Lett. 358, 199-204, 1995  
A/Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold or salinity stress in *Arabidopsis thaliana*.  
A/Reference number: 568462; MUID:95129712; PMID:7828736  
A/Accession: 568463  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residue: 1-471 «K1Z»  
A/Cross-references: UNIPROT:Q39303; UNIPARC:UPI000016DAA6; EMBL:D42061;  
RefSeq:564161; PDB:1D0086; PIR:PIR067795  
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F:138-395/Domain: protein kinase homology «K1N»  
F:146-154/Region: protein kinase ATP-binding motif

Query Match 19.2%; Score 566; DB 2; Length 471;  
Best Local Similarity 32.7%; Pred. No. 5.4e-17;  
Matches 128; Conservative 79; Mismatches 142; Indels 42; Gaps 9;

Qy	15	QSSVFLSCPTSPSMRYRTQTSSTFPPIPGSRQGPAMQDTAAAPRP-----GAGSLQHAQP	70
Db	96	EDSVOLVECVGEGRSIKNDEFS-----GNDTDSKRSPEEVSQVGI-----	137
Qy	71	PPQPRKRPEDPFKFKILGGSPSTVVLARELASSVYKILKLRHIIKNNKVPYVTR	130
Db	138	-----SDPFLKRVGGQAPGKVTQVRKDTSSIIYAKKVRKDKIKVEGSHABYKAS	188
Qy	131	RDVMSKSPFVKVLYFTPDDBKLYFLGSLYAGNKLKSLIKIGISPDSTCFATPIATV	190
Db	189	RDILTIKIDPFVGLVYSFTQVYKILVLPIDNGLFPOLYHGFPSDLALVITATV	244



Qy 72 POPRIQRDPEDPFGKIKLGGDSFETVVLKRLAETSRYSATIKILKHQHIKHNKVPYTPTR 131  
Db 21 PAPINAGLGLDSEPRKIKTGGTSGFRVMLVHKHAKTCTQYAMKILDQKRVVLLKQIKSHLNSK 80

Qy 132 DVMSRLDHPFVVKLYPTFPQDEKILYFGLSYANKGLLKYIRKIGSPDSTCTRPYATSAIVS 191  
Db 80 RLIOAVNPPFVVLKLFSPKNSHLVMYGVTVGDFPGLRIKQSPFPHARYPAAGIIVL 140

Qy 192 ALEYLHGKILIHRLDQFKNILLLNHDGHIITDTPQATVLSPEKQKRAANSVPYQATVSP 250

Db 141 TPEYLSLGLIYRDLKPNLLIDHQYIQVTDGFAKRV-----KQRTWLTQTPSYLAP 195  
 Qy 252 ELLTEKSACKSSDLALGCIYYQLVAGLPPFRAGNEYLIPOKIKLEYDPPKFPFKARD 311  
 Db 196 EILLSKGYNKAVDMALGVLIIYSMAAGYPPFFADQPIQIYSEKIVSGKVRPSPHSSDLKD 255  
 Qy 312 LVEKLLVLDAIKRLGCEMSGYGPKAHPFFESVTWENLHQQTTPKLTAYLPAM-SEDD 369  
 Db 256 LLRNLLQVLDLTKRFG-NLKNQVSDIKTHKWFATTDMIAIYQR---KVEAPPPIKFRGSGD 311  
 Qy 370 EDCYGYND 377  
 Db 312 TSNFDYD 319

RESULT 14  
 I38121  
 protein kinase - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
 C:Accession: I38121  
 R:Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.; Ludecke, H.J.; Claussen, U.; Scherer, G.; Rappold, G.  
 Hum. Mol. Genet. 4, 869-878, 1995  
 A>Title: The human protein kinase gene PKC1 on Xp22.3 displays Xp/Yp homology and is a site of chromosomal instability.  
 A:Reference number: I38121; MUID:95360006; PMID:7633447  
 A:Accession: I38121  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-358 <RES>  
 A:Cross-references: UNIPROT: P51817; UNIPARC: UP1000000D998; EMBL: X85545; NID: g1052736; PIDN: CAA59733.1; PID: g1052737  
 C:Genetics:  
 A:Gene: PKC1  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 F:47-303/Domain: protein kinase homology <KIN>  
 Query Match 19.1%; Score 560.5; DB 2; Length 358;  
 Best Local Similarity 36.6%; Pred. No. 7.2e-17;  
 Matches 123; Conservative 63; Mismatches 119; Indels 31; Gaps 6;

Qy 37 TTPGIPGSGROGPMDDTAASPRGAGSLQHAQPPQPRKPKPEDFKFGKILGEGSFSTV 96  
 Db 23 TPDGAP-----ALCPSPREALS-----PEPPVYSLQDPDTLATVGTGTGGRV 63  
 Qy 97 VLARELSATREYAIKILSKRHIIKENKVPYVTRERDMSRLDHPFVKLYPTFQDDEKLY 156  
 Db 64 HLVIKETAHGFALKVMSIPDVIIRKQEQHVNHSKSVLKEVSHPLIRLPWTHDSRFLY 123  
 Qy 157 FGLSYAKGKGLLYIRKIGSFDTCTRPYTAIVSALSYLHGKGIHRDLKPNILLNED 216  
 Db 124 MLMEYVPGSLPSYLRNKRGRFSSTGLPYSAEIIICALSYLHSGKIVYRDLKPNILLRD 183  
 Qy 217 MHQITDPTGAKVLSPEKQARANSFVGTAAQVYSPPELLTEKSACKSSDLALGCIYYQLV 276  
 Db 113 TPEYLSLGLIYRDLKPNLLIDHQYIQVTDGFAKRV-----KQRTWLTQTPSYLAP 208

Qy 72 PQRKPKPEDFKFGKILGEGSFSTVVLARELSATREYAIKILSKRHIIKENKVPYVTRER 131  
 Db 34 PPSNAGLEDFERKKTLOTGSGRVMVLVGHKATEQYAMKILDKQKVVKLKQIBHTLNEK 93  
 Qy 132 DVMSRLDHPFVKLYPTFQDDEKLYFGLSYAKGKGLLYIRKIGSFDTCTRPYTAIVS 191  
 Db 94 RILQAVEFPFLVRLYESFKDNSLTMVMBYVPGSGMPSHLRIRGRFSPHARPYAAQIVL 153  
 Qy 192 ALEYLHGKGIHRDLKPNILLNEDMHQITDPTGAKVLSPEKQARANSFVGTAAQVYSP 251  
 Db 154 TPEYLSLGLIYRDLKPNLLIDHQYIQVTDGFAKRV-----KQRTWLTQTPSYLAP 208  
 Qy 252 ELLTEKSACKSSDLALGCIYYQLVAGLPPFRAGNEYLIPOKIKLEYDPPKFPFKARD 311  
 Db 209 EILLSKGYNKAVDMALGVLIIYSMAAGYPPFFADQPIQIYSEKIVSGKVRPSPHSSDLKD 268  
 Qy 312 LVEKLLVLDAIKRLGCEMSGYGPKAHPFFESVTWENLHQQTTPKLTAYLPAM-SEDD 369  
 Db 269 LLRNLLQVLDLTKRFG-NLKNQVSDIKTHKWFATTDMIAIYQR---KVEAPPPIKFRGSGD 311  
 Qy 370 EDCYGYND 377  
 Db 325 TSNFDYD 332

Search completed: June 27, 2006, 01:37:05  
 Job time : 44 secs

Db 184 GHKLTDGPGAKGLVD-----RTMTLOOTPSYLAPEVIQSGKHGRAVDMALGILIFEML 238  
 Qy 277 AGLPPFRAGNEYLIPOKIKLEYDPPKFPFKARDLVEKLLVLDAIKRLGCEMSGYGVL 336  
 Db 239 SGFPPFPDDNPFQIYQKILAGKIDFPRHLDPHVKLLIKLLLVORTERLG-NUGKANDV 297  
 Qy 337 KAHPPFESVTWENLHQQTTPKLTAYLPAMSEDD 370  
 Db 298 KHRWFRFVDMVAVPQRKLKP-----IVPKIAGDGD 329

RESULT 15  
 OKHYCB  
 protein kinase (EC 2.7.1.37), cAMP-dependent, beta catalytic chain - Chinese hamster  
 C:Species: Cricetulus griseus (Chinese hamster)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: A40384  
 R:Howard, P.; Day, K.H.; Kim, K.B.; Richardson, J.; Thomas, J.; Abraham, I.; Fleischmann, R.D.; Gottesman, M.M.; Maurer, R.A.  
 J. Biol. Chem. 266, 10189-10195, 1991  
 A>Title: Decreased catalytic subunit mRNA levels and altered catalytic subunit mRNA structure in a cAMP-resistant Chinese hamster ovary cell line.  
 A:Reference number: A40384; MUID:91244783; PMID:1645343  
 A:Accession: A40384  
 A:Molecule type: mRNA  
 A:Residues: 1-351 <HOW>  
 A:Cross-references: UNIPROT: P05206; UNIPARC: UP1000000408F; GB: M63312; NID: g191176; PIDN: AAA37011.1; PID: g191177  
 C:Comment: The inactive enzyme contains two regulatory chains and two catalytic chains. Activation by cAMP produces two active catalytic monomers and a regulatory dimer that binds four cAMP molecules. Two types found in mammalian tissue are distinguished by having either type I or type II regulatory chains.  
 C:Comment: Both alpha and beta catalytic chains are found in many tissues, with the alpha form being the more abundant. The highest concentrations of the beta form are found in brain.  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 C:Keywords: ATP; blocked amino end; cAMP binding; heterotetramer; lipoprotein; magnesium; myristylation; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase  
 F:2-351/Product: protein kinase, cAMP-dependent, beta catalytic chain #status predicted <MAT>  
 F:42-298/Domain: protein kinase homology <KIN>  
 F:50-58/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:3/Modified site: aspartic acid (Asn) #status predicted  
 F:55,56,122,128,171,184/Binding site: Mg-ATP (Phe, Gly, Glu, Glu, Thr) #status predicted  
 F:73,92,167,169/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:172,185/Binding site: magnesium (Asn, Asp) #status predicted  
 F:198/Binding site: phosphate (Thr) (covalent) #status predicted  
 F:339/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 19.0%; Score 558.5; DB 1; Length 351;  
 Best Local Similarity 36.7%; Pred. No. 0.5e-17;  
 Matches 113; Conservative 66; Mismatches 118; Indels 11; Gaps 5;

Db 392 -SRWQDPLEPGESVVLISKLKINK--LTNKKVQLILTQKPOLICVDPGKQVTKGNIMW 447

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RESULT 7
US-10-953-349-17750
; Sequence 17750, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING
POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 3750-1528RUS2

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Db 616 -----BFDSSDMSGLSGSSSSCV-----SNHODMGDESSGFTFR 651

Qy	76	XQJPEDFKFKILBEGSPSTVVLARELSATSEYAKIKILEKXHIH1KENKVYPTVRDVM5	135
Db	244	KVLELDFELLKVLARGSPGVKMGVKKGTGKIFAMKILKQRAIIARNOVBSTKASRKILQ	303
Qy	136	RLDXPFFVKLYPTFQDDREKLYPGLSYAKQKELLYIRKIGSPDSTCTRFTYATSVSALEY	191
Qy	304	ALQHPHKLRLTARFQSPSEKILYPLVDQYQGLGEPHLKKNKRPPGEDVARIYVGEIAAALG	363
Qy	196	LHGKQI1HRLDKPKNILNEDMHIQ1DTQTKVLSPESKOQARNSPQAQTVPSRLLAT	255
Db	364	LHSLGVIYRLDKPKNILNDDINGHCLDTQGLSKVDVDSPK--AHTFGTTPYLAPBIYT	420
Qy	256	EKSACKSSDLWALGCI1YQVLQALPPFRAGNEYLI1FKQI1KLEYPFPEKFPFKARDLVEK	315
Qy	421	GAGHDKAVDWMSGLI1LYLFTVGII1PPYBQVNSKYNKIKHGVLRRPFFLSEGCKSLIVA	480
Qy	316	LLVLDTATKRLGCEMEHYGPKLKAHPFSPSTWENLHQ--QTPPKLTYAMPSSDDSDC	372
Qy	481	LLNRDPAKRLG--SGKLDLVKSHAPFKDLMDQMKREIEVP-----YKPKYSGDDT-	532
Qy	373	YGNVDNLLSGFQCMQVSSSSSSHSLSASDTGLPQSGSRIEYI1HDLNSPFLDQLFSE	432
Db	533	QNFDTPTTKPEV--VDSHVPTSKLTETVTNEP-----DAPK-DPTFOQ	572
Qy	433	DKRLL	438
Db	573	NSKIL	578

[illegible]

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Qy      3  RTTGLVLDYAPVIGSSVVLCSCPSPMVRTTTESTPPOIGGSRGGPAMDQTAAB-PRPG  61
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      305  RDTQEIFRSGPVWELGL-----PCSIQR-----ARRPCLPTPKQRP--QOISWESPLDE  352

Qy      62  AGSLGHQAPPPQAKKRP-----EDFKPGKILGEGSFVTVLARELATSRYVAKIL  113
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      353  VDKJCL-PEPELHKRPSLQIKLIKIEDPLAHKLQKSGPGVGLAFKFKTNPPAFKAL  411

Qy      114  EKRHIKENKVPVYTKRSDVMS-RLDHPFVFKLYPTFODDEKLFGLSYAKNGELLYKIR  172
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      412  KDDVVLADDVECTVSKRVLSLAWHPFLTHMCTPTQTKRNLFPVBYLAKGGDLYMHIQ  471

Qy      173  KIGSPDECTRTPTABISALEYLAHQDIIHRDLKPENILANSDHMQIITOPATAKVLSP  232
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      63KFPGLSDPVTYABIILGLQLPASKIIVYRDLKLHLLDLDKQIKIADPGMK--  520

Qy      233  ESK--QARANSFVGTAYVSPLELLSCKSSDALMGCIILYOLVGLPFPFAGNEYIL  297
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      528  ERMGLDAKTYITFCSTPDYIAPEILLOOYKNSVDMVSGVLLYEMKLGOSPFHGDSEEL  584

```

Qy	73	QPRKQRPEDIPKFKLGGSGSTVTVLARELTSREVAIKILKSKHIIKENKVPYTVRED	132
Db	107	QRKQKQVDFPELLTIIIGRGAFGFVRLCEKASIKQVYAKKGLKQKSDLRGGQVSHVYKASN	166
Qy	133	VNSRLCHPFFVKIYPTFDDEKLYGLFSYAKGKGLKYIKIKGSPDSTCFPTATIAIVSA	192
Db	167	LIAVDSAPFVLYKQFDESDYLLIKSYLGGDQVLLKGLLRGLTDEDSAPYIAETVLA	226
Qy	193	LEYLHGKGIHRLDKENILNEDHGIQITQPTGAKVLS	231
Db	227	TSIHGHSYIHRIKPNLLDORSCHLKLGDGLGCLPLDSSNPPNLNEPDYTSKTKFGL	286
Qy	232	PES-----KQARSNPVQTQGVPELLTEKACKSSDLAL	268

Search completed: June 27, 2006, 01:52:10  
Job time : 20 secs

Job time : 20 sec

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